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indolicidin precur
E2 glycoprotein pr
hypothetical prote
ACONF-13 protein
ACMNNY Orfil Bom
ATP Synthase F0 ch
hypothetical prote
bone morphogenetic
ORF MSV076 probabl
hypothetical prote
probabl glycosylt
ferredoxin-NADP re
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104.437 Million cell updates/sec
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H+-transporting t
ATP synthase F0
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H+-transporting
H+-transporting
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H+-transporting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical
                                                                                                                                                                                                                                                                                                              Description
                                             4, 2004, 15:15:37 ; Search time 11.9737 Seconds
                                                                                                                                            283366
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                             283366 seqs, 96191526 residues
                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                           T12505
E72851
T41758
E90626
AC1927
I38935
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B72392
G95922
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E89605
T29295
T11105
AH0755
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S08424
E90618
T111538
T111291
T09861
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                                                                                       1 ILPWKWPWWRR 13
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length: 2000000000
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Gapop 10.0
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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H+-transporting tw	H+-transporting tw	NADH oxidase (H2O2	hypothetical prote	integral membrane	hypothetical prote	N-acetylglucosamin	hypothetical prote	related to trfA pr	cyclic nucleotide	hypothetical prote	H+-transporting tw	H+-transporting tw	H+-transporting tw	H+-transporting tw	ATP synthase F0 ch
T11768	T11304	S23449	G70715	D87260	T18963	A54770	875101	T51071	\$70522	AB2244	S04619	T11171	T12413	E58892	E90612
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47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5		47.0	46.5	46.5		46.5	46.5
47	47	47	47	47	47	47	47	47	47	46.5	46	46	46	46	46
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ALIGNMENTS

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A; Modecule Lype: matter, A; Cross-references: EMBL: K67340; NID: 9462; PIDN: CAA47755.1; PID: 9463
A; Cross-references: EMBL: K67340; Moderies, M.L.; Tang, Y.Q.; Smith, W.; Cullor, J.S.
Biol. Chem. 267, 4292-4295, 1992
J. Biol. Chem. 267, 4292-4295, 1992
A; Title: Indolicidin, a novel bactericidal tridecapeptide amide from neutrophils. A; Reference number: A42387; MUD: 92165771; PMID: 1537821
A; Accession: A42387
A; Modesidues: 131-143 < SEL>
A; Modesidues: 131-143 < SEL>
A; Modesidues: sequence extracted from NOBI backbone (NCBIP: 83840)
C; Superfamily: cathelin; cystatin homology
C; Superfamily: cathelin; cystatin homology c785-
F; 1-29/Domain: signal sequence #status predicted < PRO>
F; 22-129/Domain: cystatin homology c785-
F; 30-130/Domain: cystatin homology c785-
F; 31-143/Product: indolicidin #status predicted < PRO>
F; 11-143/Product: indolicidin #status experimental < NATS-
F; 111-143/Modified site: amidated carboxyl end (Arg) (amide in mature form from following g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                 NiAlternate names: antimicrobial peptide
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JG1222, Ag387; S25664
R;del Sal, G.; Storici, P.; Schneider, C.; Romeo, D.; Zanetti, M.
Biochem: Biophys. Res. Commun. 187, 467-472, 1992
A;Fitle: CDNA cloning of the neutrophil bactericidal peptide indolicidin.
A;Reference number: JG1222; MUID:92392368; PMID:1520337
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.ndolicidin precursor - bovine
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nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                       A;Accession: JC1222
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Matches
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B2 glycoprotein precursor - human coronavirus (strain 229B) N;Alternate names: peplomer glycoprotein; S glycoprotein; spike glycoprotein C;Species: human coronavirus

à g RESULT 2

VGIHHC

A.Note: host Homo sapiens (man)
C.Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jun-2000
C.Accession: A34765; SO546
F.: Schelle-Prinz, B.; Siddell, S.G.
J. Gen. Virol. 71, 1065-1073, 1990

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Best Local Similarity 54.5
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-55 <KUR>
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                                                                                                                       A Molecule type: mRNA
A Residues; 1-1173 < RAA>
A Residues; 1-1173 < RAA>
A Cross-references: EMBL:X16816; NID:958926; PIDN:CAA34723.1; PID:958927
A Experimental source: Extrain 229B
A Frabbe, T.; Siddell, S.
Nucleic Acids Res. 17, 6387, 1989
A Title: Nucleotide sequence of the human coronavirus HCV 229B mRNA 4 and mRNA 5 unique
A, Reference number: A34038; MUID:8936667; PMID:2701946
A, Accession: S05460
A, Status: translation not shown
A, Molecule type: mRNA
A, Residues: 1159-1173 < RA2>
A; Cross-references: EMBL:X15654; NID:958921; PIDN:CAA33680.1; PID:91334827
C, Superfamily: ocronavirus E2 glycoprotein
C; Keywords: glycoprotein; transmembrane protein
C; Keywords: glycoprotein; transmembrane protein
F; 1-15/Domain: signal sequence #status predicted < SIG>
F; 11-113/Product: E2 glycoprotein;
F; 11-113/Product: E2 glycoprotein
F; 1116-1138/Pomain: transmembrane #status predicted < MAT>
F; 23, 62, 98, 147, 171, 176, 220, 243, 326, 333, 440, 464, 518, 538, 542, 568, 581, 587, 663, 671, 930, 1015,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACOLF.13 protein - Autographa californica nuclear polyhedrosis virus
C;Species: Autographa californica nuclear polyhedrosis virus, ACMNPV
A;Note: dSDNA virus
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 12-Nov-1999
C;Accession: E72851
R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus, A;Reference number: A72850; MUID:94303173; PMID:8030224
A;Title: Nucleotide sequence of the gene encoding the spike glycoprotein of human corona A;Reference number: A34766; MUID:90264837; PMID:2345367
A;Accession: A34766
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C,Species: Homo sapiens (man)
C,Species: Homo sapiens (man)
C,Species: Homo sapiens (man)
C,Species: Homo sapiens (man)
C,Species: Juli-1999 #sequence_revision 23-Jul-1999
C,Accession: T12505
R,Ansorge, W., Wirkner, U., Mewes, H.W., Gassenhuber, J., Wiemann, S.
Submitted to the Protein Sequence Database, June 1999
A,Reference number: Z17527
A,Reference number: Z17527
A,Residues: L299
A,Rossion: T12505
A,Rossion: T12505
A,Rossion: T1290 <ANS
A,Rossion: L299 <ANS
A,Rossion: L299 <ANS
C,Genetics: A,Rossion: A,Rossi
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Best Local Similarity 57.1%; Pred. No. 6.4;
Matches 8; Conservative 0; Mismatches 3;
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Best Local Similarity 85.7
Matches 6; Conservative
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A, Status: preliminary
A, Molecule type: DNA
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ATP Synthase FO chain 8 [imported] - Eudromia elegans mitochondrion C; Species: mitochondrion Eudromia elegans C; Species: mitochondrion Eudromia elegans C; Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 17-May-2002 C; Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 17-May-2002 R; Haddrath, O.; Baker, A.J. Froc. R. Soc. Lond. B Biol. Sci. 268, 939-945, 2001 Froc. R. Soc. Lond. B Biol. Sci. 268, 939-945, 2001 A; Reference number: A99613; MUID:21263106; PMID:11370967 Atinct birds: ratite phyloger A; Accession: E90626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:NC_002772; NID:g14141818; PIDN:NP_115277.1; GSPDB:GN00163
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleopolyhedrovirus
                                                                                                                                                                                                                                                                                                                                                                                      T41758
AcMNPV orf13 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
C;Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV
A;Variety: isolate T3
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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A;Residues: 1-327 <AYR>
A;Cross-references: GB:L22858; NID:g510708; PIDN:AAA66643.1; PID:g559082
C;Genetics:
A;Gene: Acorf-13
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R;Gomi, S.; Majima, K.; Maeda, S.
C)Gomi, S.; Majima, K.; Maeda, S.
C)Gomi, Virol. 80, 1323-1337, 1999
A;Title: Sequence analysis of the genome of Bombyx mori n A;Title: Sequence analysis of the genome of Bombyx mori n A;Title: Sequence number: Z22020; MUID:99281911; PMID:10355780
A;Accession: T41758
A;Reference number; translated from GB/EMBL/DDBJ
A;Residues: 1-331 <KAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Genome: mitochondrion
A;Genetic code: SGC1
C;Superfamily: H+-transporting ATP synthase protein
C;Keywords: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 53; DB 2;
Pred. No. 8.1;
1; Mismatches 4
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Pred. No. 2.5;
0; Mismatches
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                                                                                                                          DB 7
                                                                                                                               Score 53; DB 2
Pred. No. 8;
1; Mismatches
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54.5%;
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Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                  53.5%;
ilarity 54.5%;
Conservative
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A;Cross-references: GB:AE001713; GB:AE000512; NID:g4980809; PIDN:AAD35403.1; PID:g49808
A;Experimental source: strain MSB8
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A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: B72392
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: B7239
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL; AF063866; NID: 94049647; PIDN: AAC97813.1; PID: 94049853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORF MSV076 probable spheroidin - Melanoplus sanguinipes entomopoxvirus C; Species: Melanoplus sanguinipes entomopoxvirus C; Species: Melanoplus sanguinipes entomopoxvirus C; Jaces: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000 C; Accession: T28234
R; Afonso, C:L:; Tulman, B.R:; Lu, Z:; Oma, B.; Kutish, G.F.; Rock, D.L. J. Virol. 73, 533-552, 1999
A; Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A; Reference number: Z20484; MUID:99102612; PMID:9847359
                                    F;151-170/Domain: transmembrane #status predicted <TRM>
F;201-508/Domain: protein kinase homology <KIN>
F;209-217/Region: protein kinase ATP-binding motif
F;55,110,126/Binding site: carbohydrate (Asn) (covalent) #status
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F;27-150/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-970 <AFO>
                                                                                                                                                                                                                                DB 2;
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Pred. No. 47;
3; Mismatches
                                                                                                                                                                                                                            Score 51; DB;
Pred. No. 44;
1; Mismatches
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Pred. No. 4.9;
1; Mismatches
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57.1%;
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838 ILPYPYPWPWPYNR 851
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 8; Conserv
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NALE CRANE CALL THE SECRETOR IN RECEPTOR IN PRECURSOR - human

NALE CRANE CALL STATE OF THE NATURE (EC 2 7.1.37)

C) Date 1.6 - Feb-1906 Wasquence revision 16-Feb-1996 #text_change 24-Sep-1999

C) Species Homo sapiens (Man)

C) Date 1.6 - Feb-1906 Wasquence revision 16-Feb-1996 #text_change 24-Sep-1999

C) Address 1.6 - Feb-1906 Wasquence revision 16-Feb-1996 #text_change 24-Sep-1999

C) Address 1.6 - Feb-1906 Wasquence revision 16-Feb-1996 #text_change 24-Sep-1999

C) Address 1.6 - Feb-1906 Wasduence revision 16-Feb-1906 #text_change receptor through interaction 17-Feb-1906 Wasdadawa, N. 10-Feb-1906 
                                                                                                                                                                        A; Obte: Nostoc Sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C; Date: 14-Dec-2001 #text_change 09-Dec-2002 C; Date: 14-Dec-2001 Mill Makazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A; Reference number: AD1807; MUID:2159285; PMID:11759840
A; Reference number: AD1807; MUID:2159285; PMID:11759840
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-689 < MCNR>A; Residues: 1-689 < MCNRAPARIA </br>
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                                                                                                                                                    Species: Nostoc sp. PCC 7120
Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
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                                                                                                                hypothetical protein all0966 [imported] - Nostoc sp. (strain PCC 7120)
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Pred. No.
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Best Local Similarity
Matches 5; Conserv
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A, Reference number: S03558; MUID:89170752; PMID:2924777
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                       probable glycosyltransferase protein SMb21068 [imported] - Sinorhizobium meliloti (strai probable glycosyltransferase protein SMb21068 [imported] - Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001 C;Accession: G95922 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001 A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endc A;Reference number: A95842; MUID:21396508; PMID:11484431 A;Accession: G95922 A;Reference number: A95842; MUID:21396508; PMID:11484431 A;Accession: G95922 A;Reference: G95922 A;Reference: G95922 A;Reference: G95922 A;Residues: 1.337 <KUR>
A,Molecule type: DNA A;Residues: 1.337 <KUR>
A,Residues: 1.337 <KUR>
A,Residues: 1.337 <KUR>
A;Residues: 1.337 <KURP
A;Residues: 1.336834; PMID:11474104
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Eur. J. Biochem. 180, 479-484, 1989
A;Title: cDNA sequence of adrenodoxin reductase. Identification of NADP-binding sites in
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A;Experimental source: adrenal cortex
A;Note: the authors translated the codon GTC for residue 205 as Gly
R;Sagara, Y.; Takata, Y.; M;yata, T.; Hara, T.; Horiuchi, T.
Biochem. 102, 1333-1336, 1987
A;Title: Cloning and sequence analysis of adrenodoxin reductase cDNA from bovine adrenal A;Reference number: J10079; MUID:88198050; PMID:3448086
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A, Molecule type: mRNA
A, Coss-references: GB: D00211; NID: g217433; PIDN: BAA00150.1; PID: g217434
A, Coss-references: GB: D00211; NID: g217433; PIDN: BAA00150.1; PID: g217434
B, Sagara, Y
Submitted to DDBJ, September 1989
A, Reference number: J80390
A, Contents: revision, insertion of residues 205-210
A, Accession: J80390
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Pred. No. 19;
0; Mismatches
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Best Local Similarity 66./
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A;Residues: 56-498 <SA2>
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A;Molecule type: DNA
A,Residues: 1-498 <TAK>
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C; Genetics:
A; Gene: SMb21068
A; Genome: plasmid
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A, Resterence number: sv3238; MULD: 871/0/321; FMLD: 2344///
A, Accession: 803558
A, Molecule type: mRNA
A, Residues: 155-204,211-498 cHAN>
A, Residues: 155-204,211-498 cHAN>
A, Residues: 155-204,211-498 cHAN>
A, Cross-references: EMBL: X13766, NID: 365; PIDN: CAA32002.1; PID: 333776
A, Residues: 155-204,211-31-1988
A, Title: Adrenoferredoxin-binding peptide of NADFH-adrenoferredoxin reductase.
B, Accession: PS0003
A, Mulecule type: protein
A, Residues: 33-41/8/43-625.260-283, TW, 1496-498 cHAM>
A, Molecule type: protein
A, Residues: 33-41/8/43-625.260-283, TW, 1496-498 cHAM>
A, Molecule type: Commun. 145, 1239-1247, 1987
B, Nonaka, Y, Murakami, H., Yabusaki, Y.; Kuramiteu, S.; Kagamiyama, H.; Yamano, T.; Ok
B, Nonaka, Y, Murakami, H., Yabusaki, Y.; Kuramiteu, S.; Kagamiyama, H.; Yamano, T.; Ok
A, Title: Molecular cloning and sequence analysis of full-length cDNA for mRNA of adrenc
A, Reference number: A29604; MUID: 87270696; PMID: 3038094
A, Accession: A29604
A, Molecule type: mRNA
A, Cross-references: GB: MI7029; NID: 9162628; PIDN: AAA30362.1; PID: 9162629
A, Experimental source: adrenal cortex
B, Marburton, R. 13, Saybert, D. M.
B; Marburton, R. 13, Saybert, D. M.
A, Reference number: S52100; MUID: 95110846; PMID: 7811729
A, Reference number: S52100; MUID: 95110846; PMID: 7811729
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A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
C; Comment: Ferredoxin-NADP+ reductase is localized in the matrix of adrenal cortex mitc
erredoxin-NADP+ reductase, adrenodoxin and two forms of cytochrome P-450.
C; Genetics:
A; Introne: 27/1; 59/3; 91/3; 132/3; 170/3; 204/3; 246/3; 275/1; 341/3; 399/1; 456/1
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhodobacter capsulatus
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C)Species: Rhodobacter capsulatus
C)Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Aug-2002
C)Accession: T03562
R)VICEK, C., Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M.
Proc, Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A;Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsu
A;Reference number: 214955; MUID:97404404; PMID:9256491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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1; Mismatches
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   7; Conservative
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Bax-peptide precursor - Drosophila suzukii

N.Alternate names: male accessory gland peptide

N.Alternate names: male accessory gland peptide

C.Species: Drosophila suzukii

C.Species: Drosophila suzukii

R.Schmidt, T.; Choffat, Y.; Schneider, M.; Hunziker, P.; Fuyama, Y.; Kubli, E.

Insect Biochem. Mol. Biol. 23, 571-579, 1993

A.Title: Drosophila suzukii contains a peptide homologous to the Drosophila melanogaster

A.Reference number: A56547

A.Molecule: Loosophila suzukii contains a peptide homologous to the Drosophila melanogaster

A.Molecule: Loosophila suzukii contains a peptide homologous to the Drosophila melanogaster

A.Residues: A56547

A.Molecule: Loosophila affect affect extraction from NCBI backbone

A.Note: sequence modified affect extraction from NCBI backbone

A.Note: sequence extracted from NCBI backbone (NCBIN:136396)

A.Note: sequence extracted from NCBI backbone (NCBIN:136396)

A.Molec: sequence extracted from NCBI backbone (NCBIN:136396)
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: E84631
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; euss, D.; Mierman, W.C.; White, O.; Eisen, J.A.; Salabbrg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Residues: preliminary
A;Residues: 1-425 <STO>
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A, Residues: 20-60 <802>
A, Residues: 20-60 <802>
A, Rote: sequence modified after extraction from NCBI backbone C, Genetics:
A, Gene: FlyBase: Dsuz/SP
A, Cross-references: FlyBase: FBgn0012991
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C;Keywords: neuropeptide
F;I-19Domain: signal sequence #status predicted <SIG>
F;20-60/Product: sex-peptide #status experimental <MAT>
                           Score 49.5; DB
Pred. No. 20;
3; Mismatches
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A,Map position: 2
C,Superfamily: serine carboxypeptidase
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Best Local Similarity 50.0%;
Matches 7; Conservative
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Best Local Similarity 50.0%;
Matches 9; Conservative
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version 5.1.6
- 2004 Compugen Ltd.
GenCore
Copyright (c) 1993
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OM protein - protein search, using sw model

Мау Run on:

4, 2004, 15:08:51 ; Search time 8.21053 Seconds (without alignments) 82.444 Million cell updates/sec

Title: Perfect score:

US-09-444-281-85 99 1 ILPWKWPWWRR 13 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE=Bone marrow;
MEDLINE=92382368; PubMed=1520337;
MEDLINE=92382368; PubMed=1520337;
del Sal G., Storici P., Schneider C., Romeo D., Zanetti M.;
del Sal G., Storici P., Schneider C., Romeo D., Zanetti M.;
mcDNA cloning of the neutrophil bactericidal peptide indolicidin.";
Biochem. Biophys. Res. Commun. 187:467-472(1992).
                    01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Indolicidin precursor.
Bos taurus (Bovine).
Bustaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Rovidae; Bovinae; Bos.
111 TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Neutrophils;
MEDLINE=92165771; PubMed=1537821;
Selsted M.E., Novotny M.J., Morris W.L., Tang Y.-Q., Smith W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Indolicidin, a novel bactericidal tridecapeptide amide from neutrophila.";
"Indolicidin, a novel bactericidal tridecapeptide amide from neutrophila.";
"J. Biol. Chem. 267:4292-4295(1992).
"I. FUNCTION: Potent microbicidal activity, active against Staphylococcus aureus and Eschericida coll.
"ITSSUE SPECIFICITY: Large granules of neutrophils.
"SIMILARITY: Belongs to the cathelicidin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; JC1222; JC1222.

PDB; 1G89; 17-JAN-01.

PDB; 1HR1; 31-DEC-02.

PDB; 1HR1; 31-DEC-02.

PERM; PF0066; Cathelicidin.

ProDom; PF0066; Cathelicidin; 1.

ProDom; PF0066; Cathelicidin; 1.

PROSITE; PS00946; CATHELICIDINS 1; 1.

PROSITE; PS00947; CATHELICIDINS 2; 1.

Antibiotic; Amidation; Signal; Pyrrolidone carboxylic acid;
144 AA
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STANDARD;
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    TAKE BERREAR B
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Bonavia A., Holmes K.V.;
Wiral and cellular changes in a human cell line persistently infected with human coronavirus HCoV-229E.";
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MEDILINE-89366667; PubMed=2701946;
Raabe T., Siddell S.,
"Nucleotide sequence of the human coronavirus HCV 2295 mRNA 4 and mRNA
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                        MEDILINE=90264837; PubMed=2245367;
Raabe T., Schelle-Prinz B., Siddell S.G.;
"Nuclectide sequence of the gene encoding the spike glycoprotein of
"Nuclectide sequence" Tri Prinz HCV 229E ";
J. Gen. Virol. 71:1065-1073(1990).
         INDOLICIDIN
PYRROLIDONE CARBOXYLIC ACID (BY
SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
AMIDATION (6-144 PROVIDE AMIDE GROUP).
EBBICBBESSC09911 CRC64;
                                                                                                                                                                                                                                                                                 Human coronavirus (strain 229E) (HCOV-229E).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                    human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22440020; PubMed=12551991;
Bonavia A., Zelus B.D., Wentworth D.E., Talbot P.J., Holmes K.V.;
                                                                                                                                                                                                                                                              (Peplomer protein)
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P15423; P89342; P89343; P89344; Q66174; Q990M1; Q990M2; Q990M3;
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                                                                                        Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21262210; PubMed=11369870;
Thiel V., Herold J., Schelle B., Siddell S.G.;
"Infectious RNA transcribed in vitro from a cDNA copy of coronavirus genome cloned in vaccinia virus.";
J. Gen. Virol. 82:1273-1281(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 98-1113 FROM N.A., AND VARIANTS.
STRAIN=Isolate RW Stock, Isolate P100E, Isolate P11A, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 98-1113 FROM N.A., AND VARIANTS.
STRAIN=Isolate ATCC VR-74, Isolate A162, and Isolate LRI
MEDLINE=99086140; PubMed=9870593;
Hays J.P., Myint S.H.; S.H.; Beries of geographically and chronologically distinct human coronaviruses 229E.";
J. Virol. Methods 75:179-193(1998).
                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                        Score 99; DB 1; I
Pred. No. 5.6e-06;
                                                                                                                                                                                                                                                               glycoprotein precursor (Spike glycoprotein)
                                                                                                                                                                                                                                01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                            Mismatches
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Nucleic Acids Res. 17:6387-6387(1989).
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es 13; Conserv
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SEQUENCE F
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                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILINE=211090055; PubMed=11162792;

MEDILINE=211090055; PubMed=11162792;

Gallagher T.M., Buchmeier M.J.;

"Coronavirus spike proteins in viral entry and pathogenesis.";

Virology 279:371-374(2001).

-I- FUNCTION: Structural protein that makes spikes at the surface of the virus. Determines enteropathogenicity and virulence of the virus. Initiates infection by specifically recognizing and binding the human aninopeptidase ANPEP receptor. Its association with ANPEP may lead to its conformational change that triggers fusion between viral and host cellular membrane.

-I- SUBUNT: Homotrimer. During virus morphogenesis, it is found in a complex with M and HE proteins (By similarity). Interacts with
                                                                                                                                                   Breslin J.J., Mork I., Smith M.K., Vogel L.K., Hemmila E.M., Breslin J.J., Talbot P.J., Sjoestrom H., Noren O., Holmes K.V.; Human coronavirus 229E; receptor binding domain and neutralization by soluble receptor at 37 degrees C."; J. Virol. 77:4435-4438(2003).
Identification of a receptor-binding domain of the spike glycoprotein of human coronavirus HCoV-229E."; I. Virol. 77:2530-2538(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Type I membrane protein.
DOMAIN: The spike SI domain displays the specificity for the host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Envelope protein; Transmembrane; Signal;
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COILED COIL (POTENTIAL).
LEUCINE ZIPPER-LIKE HEPTAD REPEATS.
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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                                                                                                                                             MEDLINE=22521439; PubMed=12634402;
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InterPro, IPR002551; Corona_S1.
InterPro, IPR002552; Corona_S2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF344186; AAG48592 1; -. EMBL; AF344186; AAK32188 1; -. EMBL; AF344187; AAK32189 1; -. EMBL; AF344189; AAK32190 1; -. EMBL; AF344189; AAK32191 1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, Y09923; CAA71056.1; -. EMBL, Y10051; CAA71146.1; -. EMBL; Y10052; CAA71147.1; -. EMBL; X15654; CAA33680.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X16816; CAA34723.1; ~.
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Pfam; PF01600; Corona_S1; 1
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Coiled coil.
                                                                                                                  INTERACTION WITH ANPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01601; Corona_
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FT VARIANT 775 A -> S (in isolat.	Query Match 54.5%; Score 54; Best Local Similarity 85.7%; Pred. No. 1	Matches 6; Conservative 0; Mismatches	1113 KWPWWVW		SULT 3 13_NPVAC	ID Y013_NPVAC STANDARD; PRT; 327 AA. AC P41423;		01-NOV-1997 (Rel. 35, Last annotation Hypothetical 38.7 kDa protein in PK1	Autographa californica nuclear polyhedrosi viruses no bwa etane Bach	OC Nucleopolyhedrovirus.					RL Virology 202:586-605(1994).		STRAIN=L1;			involved in late and very late gene J. Virol. 67:3481-3488(1993).			the European Bioinformatics Institute. The		entities requires a license agreement (See ht					t c]	Pred. No. 1; Mismato	11 WEWNEW 11		Db 1 MLSWLWNWWW 11	RESILT 4	JMAN JMAN	BMKZ HUMAN SIANDAKU; FKI; 1038 013873; 016569;	DI 16-OCI-2001 (Rel. 40, Lieaceu) DI 16-OCI-2001 (Rel. 40, Last Bequence update) DI 15-MND-20004 (Pel 43 Tast annotation undate)	Bone morphogenetic protein	(PWF type il receptor)
CYS-RICH.	N-LINKED (GLCNAC) (POTENTIAL). N-LINKED (GLCNAC) (POTENTIAL). N-LINKED (GLCNAC) (POTENTIAL).	N-LINKED (GLCNAC) (POTENTIAL). N-LINKED (GLCNAC) (POTENTIAL). N-LINKED (GLCNAC) (DOMENHIAL).	LCNAC) (LCNAC) (LCNAC) (LCNAC) (N-LINKED (GLCNAC) (POTENTIAL). N-LINKED (GLCNAC) (POTENTIAL).	LCNAC	LONAC) (LCNAC)	LCNAC)	LCNAC) (N-LINKED (GLCNAC) (POTENTIAL). N-LINKED (GLCNAC) (POTENTIAL).	LCNAC) (CCNAC)	N -> S (in isolate LRI 281). N -> T (in isolate LRI 281)	LR -> IS (in isolate A162).	N -> T (in isolate P100E). T -> S (in isolate A162).	T -> N (in isolate A162).	$DF \rightarrow V$ (in isolate A162). $C \rightarrow L$ (in isolate LRI 281).	C -> F (in isolates RW Stock, P11A, P11B, P100R and AMCC VR-74)	S -> A (in isolate A162).	V -> A (in isolate LRI 281),	$T \rightarrow M$ (in isolate P100E).	n isolate A162).	GGKCFNCYPAG -> VGRCYNCRPAV (in isolate A162).	<pre>K -> N (in isolate LRI 281). KYVAVYANVG -> OFVGAKFD (in isolate A162).</pre>	V -> M (in isolate A162).	S -> T (in isolate P100E).	G -> V (in isolate Al62). Q -> K (in isolate Al62).	$V \rightarrow A$ (in isolate LRI 281). $D \rightarrow N$ (in isolate A162).	$V \rightarrow I$ (in isolate A162).	K -> N (in 1solate A162).	$L \rightarrow M$ (in isolate A162). I -> T (in isolate P11A).	V -> G (in isolate P11B).	1-11-	isolate isolate:	isolate LRI 281).	ISOLATES KW	V -> A (in isolate Al62).
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on.";
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.fornica nuclear
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virus (AcMNPV).
                         Length 1173;
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Altschul S. Peingold E. A., Grouse L. H., Derge J. G.,
Strausberg R. L., Peingold E. A., Grouse L. H., Derge J. G.,
Altausner R. D., Collins F. S., Wagner L., Shenmen C. M., Schuler G. D.,
Altschul S. F., Zeeberg B., Butcow K. H., Schaefer C. F., Bhat N. K.,
Altschul S. F., Zeeberg B., Butcow K. H., Schaefer C. F., Bhat N. K.,
A Altschul S. F., Zeeberg B., Butcow K. H., Schaefer C. F., Bhat N. K.,
B. Stapleton M., Soares M. B., Panner T. L., Scheetz T. E.,
B. Stapleton M., J. Usdin T. B., Toshiyuki S., Carninci P., Prange C.,
B. Brownstein M. J., Usdin T. B., Toshiyuki S., Carninci P., Prange C.,
B. Bosak S. A., Loquellano N. A., Peters G. J., Malek J. A., Gunarane P. H.,
Richards S., Morley K. C., Hale S., Garcia A. M., Gay L. J., Hulyk S. W.,
Villalon D. K., Muzny D. W., Sodergen E. J., Lu X., Gibbs R. R.,
Antillon D. K., Muzny D. W., Sodergen E. J., Lu X., Gibbs R. R.,
Antillon D. K., Muzny D. W., Green E. D., Dickson W. C.,
Blakesley R. W., Touchman J. W., Green E. D., Dickson W. C.,
Butterfield Y. S. N., Krzywinski M. I., Skalska U., Smailus D. E.,
Chnerchion and initial analysis of more than 15,000 full-length
F. Fro., Natl. Acad. Sci. U.S. A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS PPH1 TYR-60, TYR-117 AND ARG-483.
MEDLINE=20473811; PubMed=11015450,
Thomson J.R., Machado R.D., Pauciulo M.W., Morgan N.V., Humbert M.,
Elliott G.C., Ward K., Yacoub M., Mikhail G., Rogers P., Newman J.H.,
Wheeler L., Higenbottam T., Gibbs J.S.R., Egan J., Crozier A.,
Peacock A., Allcock R., Corris P., Loyd J.E., Trembath R.C.,
Nichols W.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95197572; PubMed=7890683; Kawabata M., Chytlin A., Moses H.L.; "Cloning of a novel type II serine/threonine kinase receptor through interaction with the type I transforming growth factor-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS PPH1 GLN-491 AND TRP-491.
MEDLINE=20395844; PubMed=10903931;
Deng Z., Morse J.H., Slager S.L., Cuervo N., Moore K.J., Venetos G.
Kalachikov S., Cayanis E., Fischer S.G., Barst R.J., Hodge S.E.,
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUB-Skin fibroblast;
TESUB-SKin fibroblast;
Nobno T., Ishlkawa T., Salto T., Hosokawa K., Noji S., Wosing D.H.,
Rosenbaum J.S.;
                                                                                                                          SEQUENCE FROM N.A.

TISSUE=Substantia nigra;

TISSUE=95372334, PubMed=7644468;

Rosenzweig B.L., Imamura T., Okadome T., Cox G.N., Yamashita H., ten Dijke P., Heldin C., Miyazono K.;

"Cloning and characterization of a human type II receptor for bone
                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification of a human type II receptor for bone morphogenetic protein-4 that forms differential heteromeric complexes with bone morphogenetic protein type I receptors.";

J. Biol. Chem. 270:22522-22526(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Familial primary pulmonary hypertension (gene PPH1) is caused by mutations in the bone morphogenetic protein receptor-II gene."; Am. J. Hum. Genet, 67:737-744 (2000).
BMPR2 OR PPH1.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                              morphogenetic proteins.";
Proc. Natl. Acad. Sci. U.S.A. 92:7632-7636(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 270:5625-5630(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                   NCBI_TaxID=9606;
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SEQUENCE FROM N.A.

MEDLINE=99416451; PubMed=10486983;

Hughes J.M., Baker A.J.;

Hughes J.M., Baker A.J.;

"Phylogenetic relationships of the enigmatic hoatzin (Opisthocomus hoazin) resolved using mitochondrial and nuclear gene sequences.";

Mol. Biol. Evol. 16:1300-1307(1999).

-! FUNCTION: This is one of the chains of the nonenzymatic component (CFC) subunit) of the mitochondrial ATPase complex.

-! CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate + H(+)(Out).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE=87270696; PubMed=3038094;
Nonaka Y., Murakami H., Yabusaki Y., Kuramitsu S., Kagamiyama H.,
Yamano T., Okamoto M.;
"Mollecular cloning and sequence analysis of full-length cDNA for mRNA
of adrenodoxin oxidoreductase from bovine adrenal cortex.";
Biochem. Biophys. Res. Commun. 145:1239-1247(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
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**SQUENCE FROM N.A., AND PARTIAL SEQUENCE.

**MEDLINE=88198050; PubMed=3448086;

**Sagara Y., Takata Y., Miyata T., Hara T., Horiuchi T.;

**Sagara Y., Takata Y., Miyata T., Hara T., Horiuchi T.;

**Cloning and sequence analysis of adrenodoxin reductase cDNA from
                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POBIG5; Q95KN8;
01-AMG-1988 (Rel. 08, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-MRR-2004 (Rel. 43, Last annotation update)
NADPH:adrenodoxin oxidoreductase, mitochondrial precursor
(BC 1.18.1.2) (Adrenodoxin reductase) (AR) (Perredoxin-NADP(+)
                                                                                                                                                                                                                                                                                                            EMBL; AF168039; AAD56467.1; -.
InterPro; IPR001411; ATPase8 mit.
Efam; PR00895; ATP-synt 8; I.
Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
SEQUENCE 55 AA; 6485 MW; 973552DB00E918AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 50, DB 1; Length 55;
Pred. No. 2.1;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLUIAR LOCATION: Membrane-bound.
-1- SIMILARITY: Belongs to the ATPase protein 8 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     492 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                         BONE MORPHOGENETIC PROTEIN RECEPTOR TYPE
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PROSITE; PS00108; PROTEIN_XINASE_ST; FALSE_NEG.

PROSITE; PS50011; PROTEIN KINASE_DOM; 1.

Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;

Reansmembrane; Glycoprotein; Signal; Polymorphism; Disease mutation.

SIGNAL
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Archosauria, Aves, Neognathae, Musophagiformes, Musophagidae,
                                                                                                                                                                                                                                                     (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
MTATPS OR ATP8.
CCTYthaixoides concolor (Grey go-away-bird).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AR 013677.
(in PPH1; sporadic).
AR 013678.
(in PPH1; complete loss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 1038;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VAR 013679.

R -> Q (in PPH1; sporadic)

/FTId=VAR 013680.

R -> W (in PPH1).
                                                                                            II.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                 CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
                                                                                                                                             PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VAR_013673.
C -> S (in PPH1).
/FTId=VAR_013674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C -> Y (in PPH1).
/FTId=VAR_013676.
C -> R (in PPH1).
/FTId=VAR_013677.
                                                                                                                                                                                                                                                                                                      _____VAR 013670.
C -> Y (in PPH1).
/FTId=VAR 012
                                                                                                                                                                                                                                                                                                                                           (in PPH1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTIG=VAR 013675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId=VAR 013681
K -> T (in PPH1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AR 013672 (in PPH1)
                                                                                                                                                                                                                                                                                                   (in PPH1
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POLY-SER.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 -> R (ir
/FTId=VAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D -> G (ir
function).
                                                                                                                                                                                                                         POLY-THR.
POLY-ASN.
                                                                                                                                                                                                                                                                                                                                                                                            C -> R (ir
/FTId=VAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
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Best Local Similarity 66.7
Matches 6; Conservative
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NCBI_TaxID=103956;
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NP BIND
BINDING
ACT SITE
DOMAIN
   PROSITE;
PROSITE;
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X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF COMPLEX WITH ADRENODOXIN.
MEDLINE=21264735; PubMed=11053423;
Mueller J.J., Lapko A., Bouvenkov G., Ruckpaul K., Heinemann U.;
Mueller J.J., Lapko A., Bouvenkov G., Ruckpaul K., Heinemann U.;
Madenodoxin reductase-adrenodoxin complex structure suggests electron transfer path in steroid biosynthesis.";
J. Biol. Chem. 276:2786-2789(2001).
-:-FUNCTION: Serves as the first electron transfer protein in all the mitochondrial p450 systems. Including cholesterol side chain cleavage in all steroidogenic tissues, steroid 11-beta hydroxylation in the adrenal cortex, 25-CH-vitamin D3-24 hydroxylation in the kidney, and sterol C-27 hydroxylation in the liver.
-:-CATALYTIC ACTIVITY: Reduced adrenodoxin + NADP(+) = oxidized
                                                                                                                                         SEQUENCE OF N-TERMINUS, AND PARTIAL SEQUENCE.
TISSUBE-Adrenal cortex,
MEDLINE=88080777; PubMed=3501502;
Hanukoglu I., Gutfinger T., Haniu M., Shively J.E.;
Hanukoglu I., Gutfinger T., Haniu M., Shively J.E.;
Tsolation of a cDNA for adrenodoxin reductase (ferredoxin-NADP+
reductase). Implications for mitochondrial cytochrome P-450 systems.";
Eur. J. Biochem. 169:449-455(1987).
                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
MEDLINE=20455764; PubMed=10998235;
Ziegler G.A., Schulz G.E.;
"Crystal structures of adrenodoxin reductase in complex with NADP+ and NADPH suggesting a mechanism for the electron transfer of an enzyme family.";
                                                                                                                                                                                                                                                                                     TISSUB=Adrenal gland;
MEDLINE=9929392; PubMed=10369776;
Ziegler G.A., Vonrhein C., Hanukoglu I., Schulz G.B.;
The structure of adrenodoxin reductase of mitochondrial P450 systems:
electron transfer for steroid biosynthesis.";
J. Mol. Biol. 289:981-990(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Long,
IsoId=P08165-2; Sequence=VSP_003415;
Note=Represents 10-20% of all adrenodoxin reductase mRNAs and seems to be inactive;
                           TISSUE=Adrenal cortex;
MEDLINE=89170752; PubMed=2924777;
Hanukoglu I., Gutfinger T.;
"CDNA sequence of adrenodoxin reductase. Identification of NADP-binding sites in oxidoreductases.";
Eur. J. Biochem. 180:479-484(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 33-492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochemistry 39:10986-10995(2000).
             SEQUENCE FROM N.A
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ODAYH -> RVYKLT (IN REF. 3).

K -> R (IN REF. 3).

S -> RL (IN REF. 3).

RAAGTRLAUTR -> ARRSAMGSPE (IN REF. 3).

TRAVPTGDVEDL -> HPGSAHWGCGGP (IN REF. 3).
                                                                                  (IN REF
                                                            MITOCHONDRION.
NADPH:ADRENODOXIN OXIDOREDUCTASE.
E -> EVLLLCQ (in isoform Long).
FILL—VSP 00341s.
G -> R (IN REF. 3).
FGVAPDHPEVKAVI -> VWLALITPRSRMLL
                                               Electron transport; Cholesterol metabolism; Oxidoreductase; Mitochondrion; FAD; Flavoprotein; NADP; Transit peptide; Hernative splicing; 3D-structure.

TRANSIT 1 32 HTTOCHONDRION.

CHAIN 3 492 NADPH;ADRENODOXIN OXIDOREDUCTA VARSPLIC 204 204 E -> EVLLLCQ (in isoform Long)
       PIR; TUTO751; JT0751.
PDB; ICJC; 12-ARR-99.
PDB; IEIL; 24-SEP-00.
PDB; IEIN; 24-SEP-00.
PDB; IEIN; 24-SEP-00.
PDB; IEIN; 24-SEP-00.
PDB; IEER; 24-SEP-00.
PDB; IEER; 24-SEP-00.
PDB; IEER; 24-SEP-00.
PDB; PRINTS; PRO0419; ADXRDTASE.
D00211; BAA00150.1;
X13736; CAA32002.1;
                                                                             77
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                                                                                               CONFLICT
CONFLICT
CONFLICT
CONFLICT
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EMBL, D83475; BAA11921.1; -.
EMBL, D83472; BAA11921.1; JOINED.
EMBL, D83473; BAA11921.1; JOINED.
EMBL, D83474; BAA11921.1; JOINED.
EMBL, M17029; AAA30362.1; -.
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54

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2 LPWKWPW 8
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48 MPWTWPW
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                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zardoya R.,
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: This is one of the chains of the nonenzymatic component
-(CF(0) subunit) of the mitochondrial ATPase complex.
-:- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
H(+)(Out).
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Testudines, Pleurodira, Pelomedusidae, Pelomedusa.
                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
ATP synthase protein 8 (AC 3.6.3.14) (ATPage subunit 8) (AGL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001421; ATPRase8_mit.
Pfam; PF00895; ATP-synt_8: 1.
Ptam; PF00805; ATP-synt_8: 0.
TRANGMEM 24 24 POTBNTIAL.
SEQUENCE 55 AA; 6536 MM; D8D4BC8F8651A001 CRC64;
                                                                                                                                                                                                                                                          Length 492;
                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.5%; Score 48; DB 1; Length 55; 71.4%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Wembrane-bound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pelomedusa subrufa (African side-necked turtle) Mitochondrion.
                                                                                                                                                                                                                                                         Score 50; DB 1;
Pred. No. 15;
); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                              3 PWKWPWWPW 11
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Best Local Similarity
--na 6; Conserv?
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Matches 5; Conserv
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079674;
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                                                                                                                                                                                                                                                                                                                 Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y., Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nasanari K., Masuho Y., Saski N.; "NEDO human cDNA sequencing project."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                  Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                     SECURNCE FROM N.A.
MEDLINE=20272150; PubMed=10810093;
Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;
Lai C.-H., Chou G. novel human genes evolutionarily conserved in Caenorhabditis elegans by comparative proteomics.";
Genome Res. 10:703-713(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 189.
                                                  Elongation of very long chain fatty acids protein 1 (CGI-88) ELOVL1 OR SSC1.
      Q9BWG0; Q9NVD9; Q9X396; 28-FEB-2003 (Rel. 41, Created) 29-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
279 AA
                                                                                                                                                                                                                                                                                                    TISSUE=Kidney;
MEDLINE=22388257; PubMed=12477932;
STANDARD;
                                                                   Homo sapiens (Human).
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                      NCBI_TaxID=9606;
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Gaps

.. 0

1; Indels

1; Mismatches

Conservative

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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISCUE Breast tumor;

MEDLINE = 238825; Pubmed=12477932;

MEDLINE = 238825; Pubmed=12477932;

A Klauener R.D., Colline F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abzamson R.D., Mulahy S.J.,

Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=BALB/C; TISSUE=Liver; MEDLINE=20553178; PubMed=10791983; MEDLINE=20553178; PubMed=10791983; Tvidik P., Westerberg R., Silve S., Asadi A., Jakobsson A., Loison G., Jacobsson A.; Silve S., Asadi A., Train G., Jacobsson A.; Silve S., Asadi A., Train G., Train G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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POTENTIAL.
ENDOPLASMIC RETICULUM RETRIEVAL MOTIF
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                              Genew; HGNC:14418; ELOVLI.
InterPro; IPR002076; GNS1_SUR4.
Pfam; PF0:151; ELO; 1.
PROSITE; PS01189; ELO; 1.
PROSITE; PS01189; ELO; 1.
TRANSMEM 23 43 POTENTIAL.
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B168E4C7EAF92A6 CRC64;
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20-11-21, (2910-12).
28-FEB-2003 (Rel. 41, Created).
28-FEB-2003 (Rel. 41, Last sequence update).
10-OCT-2003 (Rel. 42, Last annotation update).
11-0-OCT-2003 (Rel. 42, Last annotation update).
ELOYL: OR SSCI.
                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                    EMBL; AF151846; AAD34083.1; ALT_FRAME.
EMBL; AK001653; BAA91813.1; -.
EMBL; BC000618; AAH00618.1; -.
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es 6; Conservative
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251
277
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                                                                                         -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Potential).
-!- TISSUE SPECIFICITY: Expressed in a broad variety of tissues.
Highly expressed in stomach, lung, kidney, skin and intestine.
Moderately expressed in white adipose tissue, liver, spleen, brain, brown adipose tissue, heart and muscle. Weakly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENDOPLASMIC RETICULUM RETRIEVAL MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y.;
Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
Nature 409:685-690(2001).
Instruction: could be implicated in tissue-specific synthesis of long chain fatty acids and sphingolipids. May catalyze one or of the reduction reaction in fatty acid elongation, i.e., conversion of beta-kercacyl CoA to beta-hydroxyacyl CoA or reduction of trans-2-encyl CoA to the saturated acyl CoA
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GASALCESFDB2F76 CRC64;
                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 strity 66.7%; Pred. No. 19; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to the ELO family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL)
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InterPro; IPR002076; GNS1_SUR4.
Pfam; PF01151; ELO; 1.
PROSITE; PS01188; ELO; 1.
Fatty acid biosynthesis; Transme
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF170907; AAF72572.1; -. EMBL; BC006735; AAH06735.1; -. EMBL; AK003743; BAB22975.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32678 MW;
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Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       derivative.
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PWNWPW 54
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                                                                                                                                                                                                                                                                                                                                                        STRAIN=Norwegian coastal 1;

MEDLINE=96414925; PubMed=8817926;

Johansen S., Bakke I.;

Johansen S., Bakke II.;

Johansen S., Bakke II.;

Johansen S., Bakke II.;

Mol. Mar. Biol. Biotechnol. 5:203-214(1996).

-!- FUNCTION: This is one of the chains of the nonenzymatic component (CF(0) subunit) of the mitochondrial ATPase complex.

-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Taleostei, Euteleostei, Neoteleostei, Acanthomorpha, Paracanthopterygii, Gadiformes, Gadidae, Gadus.
                                                                                                                                                                                                                                                                                     Johansen S., Guddal P.H., Johansen T.; "Organization of the mitochondrial genome of Atlantic cod, Gadus
                                                                                                            01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-07-2003 (Rel. 42, Last annotation update)
ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (AGL).
MTATPB OR ATPB.
Gadus morhua (Atlantic cod).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X17659; CAA335655.1; -.
EMBL; X99772; CAA68110.1; -.
PIR; S08424; S08424.
Interpro; PFR001421; ATPase8_mit.
Pfam; PF00895; ATP-synt 8; 1.
Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.5%; Score 47; DB 1; Length 55; 83.3%; Pred. No. 4.9; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the ATPase protein 8 family.
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                                                                                       55 AA.
                                                                                                                                                                                                                                                                STRAIN-Norwegian coastal 1; TISSUE-Liver;
MEDLINE-90174958; PubMed-2308841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Membrane-bound.
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                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 18:411-419(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 AA; 6481 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                        STANDARD;
                      147 VLPWSW-WW 154
         1 ILPWKWPWW 9
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=S.salar; TISSUE=Liver;
MEDILIS=20018174; PUMMG=LO548724;
Hurst C.D., Bartlett S.E., Davidson W.S., Bruce I.J.;
"The complete mitochondrial DNA sequence of the Atlantic salmon, Salmo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arnason U., Johnsson E., Rasmussen A.S.;
"The complete mitcohondrial genome sequence of a teleost, Salmo salar, and comparisons with other salmoniformes.";
Submitted (WAR-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: This is one of the chains of the nonenzymatic component (CF(0) submit) of the mitcohondrial ATPase complex.
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(IN) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=0.mykiss; TISSUB=Liver;
MEDLINE=96139027; PubMed=8587139;
Zardoya R., Garrido-Pertierra A., Bautista J.M.;
"The complete nucleotide sequence of the mitochondrial DNA genome of the rainbow trout, Oncorphychus mykiss.";
J. Mol. Evol. 41:942-951(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Buteleostei, Protacanthopterygii, Salmoniformes; Salmonidae; Oncorhynchus. NCBI_TaxID=8022, 8030;
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0
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
MTATP8 OR ATP8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00895; ATP-synt_8; 1.
Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
TRANSMEM 4 24 POTENTIAL.
SEQUENCE 55 AA; 6413 MW; nonconcerved.
                                                                                                                                                                            Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri), and Salmo salar (Atlantic salmon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 1; Length 55;
Pred. No. 4.9;
0; Mismatches 1; Indels
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-1- SIMILARITY: Belongs to the ATPase protein 8 family.
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EMBL; AR133701; A.F61382.1; --
PIR; T09861; T09661
PIR; T09951; T09951
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Similarity 83.3%;
5, Conservative
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Best Local Similarity
Matches 5, Conserv
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                                                                                                                                                                                                                                               Mitochondrion.
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RESULT 12 ATP8_PRODO

55 AA

STANDARD;

RESULT 11 ATP8_ONCMY ID ATP8_ONCMY us-09-444-281-85.rsp

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#(+)(Out)
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ATP8_SALFO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei,
Protacanthopterygii, Salmoniformes, Salmonidae, Salvelinus.
                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Dipnoi, Lepidosireniformes, Protopteridae, Protopterus.
NCBI_TaxID=27779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
ATP Synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
MTATP8 OR ATP8 OR ATPASE8.
Salvelinus alpinus (Arctic char).
                                                     15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
MTATP8 OR ATP8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.5%; Score 47; DB 1; Length 55; larity 83.3%; Pred. No. 4.9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Membrane-bound.
-!- SIMILARITY: Belongs to the ATPase protein 8 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WBL; L42213, S68132, S68132.
PIR; S68122; S68132.
PIR; S68122; S701421; ATPase8 mit.
Pfam; PF00895; ATP-synt 8; 1.
Hydrogen ion transport; CF(0); Mitochondrion; 'Hydrogen ion transport; CF(0); Mitochondrion; 'Ardrogen ion transport; 'Ardroge
55 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 AA.
                                                                                                                                                                                                        Protopterus dolloi (Slender lungfish).
                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Egg;
MEDLINE=96271539; PubMed=8846902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                       Mitochondrion.
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Q9XN27;
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   ATP8_PRODO
Q35416;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: This is one of the chains of the nonenzymatic component (CF(0) subunit) of the mitochondrial ATPase complex.
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-!- PUNCTION: This is one of the chains of the nonanzymatic component (CF(0) subunit) of the mitcohondrial Arrase complex.
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
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                                                                                                                              -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
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Dolton S., Bliar P.U., Bernatchez L.;
A comparative analysis of complete sequence of mitochondrial
"A comparative analysis of complete sequence of mitochondrial
between brook char (Salvelinus fontinalis) and arctic char (S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
MTATP synthase protein 8 (EC 3.6.3.14) (Afpase subunit 8) (A6L).
MTATPS OR ATPS OR ATPASES.
Salvelinus fontinalis (Brook trout) (Brook char).
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF154850, AAD41376.1; -.
InterPro; IPR001421; ATPase8 mit.
Parm; PP00895; ATP-87NL 8; I, Mitochondrion; Transmembrane.
Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
SEQUENCE 55 AA; 6443 MW; D02930C2E346925F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF154851; AAD41389.1; -.
InterPro; IPR001421; ATPase8 mit.
Pram; PF000895; ATP-871L.8; Mitochondrion; Transmembrane.
Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
SEQUENCE 55 AA; 6455 MW; 71E430C2E346924A CRC64;
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Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47; DB 1; Length 55;
Pred. No. 4.9;
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                                                                                                                                                                                                     -!- SUBCELLUIAR LOCATION: Membrane-bound.
-!- SIMILARITY: Belongs to the ATPase protein 8 family.
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Matches 5; Conserv
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us-09-444-281-85.rsp

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C TISSUE-MAGICE,

MEDLINE-98393590; PubMed=9725850;

MEDLINE-98393590; PubMed=9725850;

A Darvier P., Laudet V., Gachelin G.;

A Jarvier P., Laudet V., Gachelin G.;

Index complete nucleotide sequence of the mitochondrial DNA of the dogfish, Scyllorhinus canicula.";

Genetics 150:331-344(1998).

C -: FUNCTION: This is one of the chains of the nonenzymatic component (CF(0) subunit) of the mitochondrial ATPase complex.

C -: CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate + H(2)O + M(2)Out).

C -: SUBCELLULAR LOCATION: Membrane-bound.

C -: SIMILARITY: Belongs to the ATPase protein 8 family.
                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
ATP synthase protein 8 (EC 3.6.3.14) (AfPase subunit 8) (AGL).
MTATP8 OR ATP8 OR ATPASES.
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       47.5%; Score 47; DB 1; Length 55; 83.3%; Pred. No. 4.9; 1; Indels cive 0; Mismatches 1; Indels
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Pred. No. 4.9;
0; Mismatches 1; Indels
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tive 0;
Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                             3 PWKWPW 8
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Search completed: May 4, 2004, 15:20:17 Job time : 9.21053 secs

49 PWNWPW 54

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Gaps
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APPLICANT: West, Michael H.P.
APPLICANT: Wieser, Michael H.P.
APPLICANT: Taylor, Robert
APPLICANT: Taylor, Michael BERY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
STATE: Washington
COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,314
FILING DATE: 20-AUG-1997
CLASSIFICATION: 424
ATTONREY/AGNET INPORMATION:
REGISTRATION NUMBER: 39,317
REGISTRATION NUMBER: 39,317
RELERANCE/DOCKET NUMBER: 660081.405
TELEFROME (206) 622-4900
TELEFRAM: (306) 632-631
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
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100.0%; Score 91, DB 3, L
Best Local Similarity 100.0%; Pred. No. 1.1e-06,
Matches 13; Conservative 0; Mismatches 0;
US-09-030-619-109
US-08-657-486-58
US-09-030-619-54
US-09-030-619-54
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US-08-030-619-110
US-08-030-619-51
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US-09-057-486-55
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US-09-057-486-56
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US-08-915-314-45
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TYPE: amino acid
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       STRANDEDNESS:
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/cgn2_6/ptcdata/2/jaa/6A_COMB.pep:*
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/cgn2_6/ptcdata/2/jaa/PcTUS_COMB.pep:*
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                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-915-314-65
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US-09-002-019-95
US-09-0030-619-95
US-09-667-486-30
US-09-667-486-63
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US-09-030-619-72
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US-09-030-619-72
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US-09-030-619-64
US-08-915-314-52
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US-08-915-314-74
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
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GENERAL INFORMATION:
APPLICANT: Frager, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: Wast, Michael H.P.
APPLICANT: Taylor, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Faffe, Douglas
TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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CITY: Seattle
STATE: Washington
COUNTRY. 98104
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/915,314
***TING DATE: 20-AUG-1997
                CONTRY: ASSET: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
STRY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER: PSDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,314
FILLING DATE: 20-AUG-1997
CLASSIFICATION: 424-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 91; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  i LOCATION: 13
; OTHER INFORMATION: /note= "D-Form of Lysine"
US-08-915-314-63
                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: No. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 66081.405
TELECOMMUNICATION INFORMATION:
TELEPANE: (206) 622-4900
TELEPANE: (206) 682-6031
INFORMATION FOR SEQ ID No: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 64, Application US/08915314
Patent No. 6180604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ILKKWPWWPWRRK 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
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                                                                                                                                                                                            GENERAL INCOMPATION:
GENERAL INCOMPATION:
APPLICANT: Krieger, Timothy J.
APPLICANT: Krieger, Timothy J.
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Erfle, Douglas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: OF INVENTION: UNECTIONS USING ANALOGUES OF INDOLICIDIN
NUMBER OF SEQUENCES: 90
GORBESPONDENCE ADDRESS:
ADDRESSEE: SEAD and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STREET: Washington
COUNTRY: USA
COMPUTER: FLORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin RC-DOS/MS-DOS
SOFTWARE: Patentin RC-DOS/MS-DOS
SOFTWARE: Patentin RC-DOS/MS-DOS
SOFTWARE: PATENTIN NUMBER: US/08/915,314
FILING DATE: 20-AUG - 1997
CLASSIFICATION: 424
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APPLICANT: West, Minacl H.P.
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Taylor, Robert
APPLICANT: Brile, Douglas
TITLE OF INVENTION: COMPOSITIONS USING ANALOGUES OF INDOLICIDIN NUMBER OF SEQUENCES: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LCCATION: 1
OTHER INFORMATION: /note= "D-Form of Isoleucine"
US-08-915-314-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: No. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                        Sequence 62, Application US/08915314 Patent No. 6180604 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 63, Application US/08915314
Patent No. 6180604
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (206) 682-6031
INPORMATION FOR SEQ ID NO: 62
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acide
TYPE: amino acid
STRANDENNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ILKKWPWWPWRRK 13
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     1 ILKKWPWWPWRRK 13
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Gaps

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Gaps

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APPLICANT: Krieger, Timothy J.
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Brife, Douglas
APPLICANT: Brife, Douglas
APPLICANT: Brife, Douglas
APPLICANT: Mest, Michael H.P.
APPLICANT: Mest, Michael H.P.
APPLICANT: Mest, Michael H.P.
APPLICANT: Mest, Michael H.P.
TITLE OF INVENTION: COMPOSITIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
TITLE OF INVENTION: WITH ANTIBIOTICS
TITLE OF INVENTION WHERE: US/09/030,619B
CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 95
LENGTH: 13
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GENERAL GENERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 13;
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                             Query Match
100.0%; Score 91, DB 3, I
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
COTHER ACTION: Cationic Peptide Analogue
US-03-030-619-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Cationic Peptide Analogue
US-09-030-619-95
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-030-619-95
; Sequence 95, Application US/09030619B
; Patent No. 6503881
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Patent No. 6503881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                1 ILKKWPWWPWRRK 13
                                                                                                                                                                                                                                                                  1 ILKKWPWWPWRRK 13
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j Sequence 36, Application US/09042071

j Patent No. 6294372

general information:

APPLICANT: Burian, Jan

APPLICANT: Burian, Jan

APPLICANT: Kay, William W.

TITLE OF INVENTION: SMALL CRYPTIC PLASMIDS AND METHODS FOR CONSTRUCTING

TITLE OF INVENTION: CONTROLLED-REPLICATION PLASMID VECTORS

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESSS:

ADDRESSEB: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CUNTRY: Meathle

STATE: Washington

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 91; DB 3; Length 13; 100.0%; Pred. No. 1.1e-06;
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MEDIUM TYPE: R10Py disk

COMPUTER READABLE FORM:

MEDIUM TYPE: R10Py disk

COMPTTER: BM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/042,071

FILING DATE: 13-MAR-1998

CLASSIFICATION: 438

ATTORNEY/AGBWT INFORMATION:

NAME: MCMASTERS, 33,963

REFERENCE/DOCKET NUMBER: 660081.407

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acide

TYPE: amino acide

STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: /note= "D-Form of Isoleucine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site
LOCATION: 13
OTHER INFORMATION: /note= "D-Form of Lysine"
                NAME: No. 6180604tenburg Ph.D., Carol REGISTRATION NUMBER: 39,317
REGISTRATION NUMBER: 39,317
REGISTRATION NUMBER: 39,317
TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID No: 64: SEQUENCE CHARACTERISTICS: LENGTH: 13 amino acids TYPE: amino acid STRANDEDNESS: TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
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US-09-042-071-36
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US-09-042-071-36
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Gaps

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RESULT 10
US-09-667-486-63
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                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING INFECTIONS USING ANALOGUES OF INDOLICIDIN
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    Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/667,486
FILING DATE: 22-Sep-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
Query Match
100.0%; Score 91, DB 4, L
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/915,314
FILING DATE: 20-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: No. 6538106tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                                                                                                                                                                                                                                               Sequence 30, Application US/09667486; Patent No. 6538106; GENERAL INFORMATION: APPLICANT: Fraser, Janet R. Krieger, Michael H.P. Krieger, Timchiy J. Taylor, Robert Erfle, Douglas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (206) 622-4900
TELEFAR: (206) 682-6031
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 62, Application US/0967486
Patent No. 6538106
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Fraser, Janet R. West, Michael H.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ILKKWPWWPWRRK 13
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                                                                                            1 ILKKWPWWPWRRK 13
                                                                                                                                      1 ILKKWPWWPWRRK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                          RESULT 8
US-09-667-486-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-667-486-62
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| Batent No. 6538106
| Parent No. 6538108
| Parent No. 6
Krieger, Timothy J.
Taylor, Robert
Erfle, Douglas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
INFECTIONS USING ANALOGUES OF INDOLICIDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: Ush

ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DAYEN
COMPUTER: IBM PC compatible
COMPUTER: DAYEN
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWAREN
SOFTWAREN
APPLICATION DAYEN
APPLICATION NUMBER: US/08/915,314
FILING DATE: 20-860-200
CLASSIFICATION OFF
APPLICATION NUMBER: US/08/915,314
FILING DATE: 20-MG(1997
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6538106temburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
TELEFONEY/AGENT INFORMATION:
TELEFONEY(2006) 622-4900
TELEFONE: (2006) 622-4900
TELEFONE: (2006) 622-4900
TELEFONE: (2006) 622-6031
INFORMATION FOR SEQIENCE: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 91, DB 4, I
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0;
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STATE: Washington
COUNTRY: USA
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APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Taylor, Robert
APPLICANT: Erfle, Douglas
TITLE OF INVENTION: OCMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Machington
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OTHER INFORMATION: /note= "D-Form of Isoleucine"
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COUNTRY:

COUNTRY:

CONDUTER:

MEDIUM TYPE:

COMPUTER:

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OTHER INFORMATION: /note= "D-Form of Lysine"
SEQUENCE DESCRIPTION: SEQ ID NO: 64:
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100.0%; Score 91; DB 4; L
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                                               REGISTRATION NUMBER: 39,317
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELEPHONE: (206) 632-4900
TELEPHONE: (206) 632-6031
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                    ATTORNEY/AGENT INFORMATION: NAME: No. 6538106tenburg Ph.D., Carol
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                             FILING DATE: 20-AUG-1997
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: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
COMPUTER READBLE FORM:
MINIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: IBM INTORMATION:
COMPUTER: IBM INFORMATION:
TELECOMMUNICATION IMPER: 660031.405
TELECOMMUNICATION IMPER: 660031.405
TELECOMMUNICATION IMPER: 660031.405
TELEPRATION IMPER: 180.60031.405
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100.0%; Score 91; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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ADDRESSES: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 13
OTHER INFORMATION: /note= "D-Form of Lysine"
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
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APPLICATION NUMBER: US/09/667,486
FILING DATE: 22-Sep-2000
FLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/915,314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 64, Application US/09667486; Patent No. 6538106; Patent No. 6538108; Patent NFORMATION: APPLICANT: Fraser, Janet R.; Krisger, Timothy J. Taylor, Robert; Erfle, Douglas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 90
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STATE: Washington
COUNTRY: USA
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US-09-667-486-64
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Length 14;

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APPLICANT: Framer, Janet R.

West, Michael H.P.

Taylor, Robert

Erfle, Douglas

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING

INPECTIONS USING ANALOGUES OF INDOLICIDIN

NUMBER OF SEQUENCES: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIOM TYPE: Floppy disk

MEDIOM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT ABLICATION DATA:

APPLICATION NUMBER: US/09/667,486

FILING DATE: 22-Sep-2000

CLASSIFICATION NUMBER: US/08/915,314

FILING DATE: 20-AUG-1997

ATTORNEY/ABOT INFORMATION:

REGISTRATION NUMBER: 660081.405

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
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Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                      100.0%; Score 91; DB 4; I 100.0%; Pred. No. 1.1e-06; Live 0; Mismatches 0;
; FEATURE:
OTHER INFORMATION: Cationic Peptide Analogue
US-09-030-619-108
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SEQUENCE DESCRIPTION: SEQ ID NO: 57:
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US-09-667-486-57
; Sequence 57, Application US/09667486
; Patent No. 6538106
; GENERAL INFORMATION:
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COUNTRY: USA
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                                                                                                                                                                                                                                                                              1 ILKKWPWWPWRRK 13
                                                                                                         Query Match
Best Local Similarity 100.
Matches 13; Conservative
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APPLICANT: Trigger, Timothy J.
APPLICANT: Trigger, Timothy J.
APPLICANT: Trigger, Taylor, Robert
APPLICANT: Erfle, Douglas
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: WHITH ANTIBIOTICS
FILE REFERENCE: 660081.406
CURRENT APPLICANTON NUMBER US(29/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SEQ ID NO 72
SEQ ID NO 72
LENGTH: 14
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Sequence 108, Application US/09030619B

Patent No. 65038B1

APPLICANT: Krieger, Timothy J.

APPLICANT: Effle, Douglas

APPLICANT: Taylor, Robert

APPLICANT: Fraser, Janet R.

APPLICANT: West, Michael H.P.

APPLICANT: OF SECOIOL NOWER: US/09/030,619B

CURRENT APPLICATION NUMBER: US/09/030,619B

CURRENT FILE OF INTO NOWER: 1998-02-25

NUMBER OF SECOIO NOS: 232

SOFTWARE: FastSEC for Windows Version 3.0
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Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                    Query Match
100.0%; Score 91; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-030-619-72
; Sequence 72, Application US/09030619B
? Patent No. 65038B1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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         amino acid
                                                               linear
                        STRANDEDNESS:
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TOPOLOGY: 11
US-08-915-314-57
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US-09-030-619-108
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LENGTH: 14
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1 ILKKWPWWPWRRK 13
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US-09-030-619-99
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Sequence 95, Appl
Sequence 95, Appl
Sequence 3, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 56, Appli
Sequence 57, Appli
Sequence 57, Appli
Sequence 58, Appli
Sequence 58, Appli
Sequence 58, Appli
Sequence 58, Appli
Sequence 56, Appli
Sequence 56, Appli
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                                                                                                  4, 2004, 15:22:18 ; Search time 37.2895 Seconds (without alignments) 96.635 Million cell updates/sec
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1. (cgn2 6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2. (cgn2 6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

3. (cgn2 6/ptodata/1/pubpaa/US06 PUBCOMB.pep:*

3. (cgn2 6/ptodata/1/pubpaa/US06 PUBCOMB.pep:*

5. (cgn2 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

6. (cgn2 6/ptodata/1/pubpaa/DEGG PUBCOMB.pep:*

7. (cgn2 6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

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8. (cgn2 6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

9. (cgn2 6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

10. (cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

11. (cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

12. (cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

13. (cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

14. (cgn2 6/ptodata/1/pubpaa/US108 PUBCOMB.pep:*

15. (cgn2 6/ptodata/1/pubpaa/US10B PUBCOMB.pep:*

16. (cgn2 6/ptodata/1/pubpaa/US10B PUBCOMB.pep:*

17. (cgn2 6/ptodata/1/pubpaa/US10B PUBCOMB.pep:*

18. (cgn2 6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

18. (cgn2 6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

18. (cgn2 6/ptodata/1/pubpaa/US60 NEW PUB.pep:*

18. (cgn2 6/ptodata/1/pubpaa/US60 NEW PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-030-619-99
US-10-277-232-99
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US-10-229-368-5
US-10-225-087-5
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                                                                                                                                                                                                                                                                                             1138120 seqs, 277189581 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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91
1 ILKKWPWWPWRRK 13
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seq length: 200000000
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        16
        91
        100.0
        13
        15
        US-10-277-233-95
        Sequence 99, Appl 100.0

        17
        91
        100.0
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        15
        US-10-351-995-30
        Sequence 99, Appl 100.0

        19
        100.0
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        15
        US-10-351-985-63
        Sequence 62, Appl 200.0

        20
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        100.0
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        US-10-351-985-64
        Sequence 63, Appl 200.0

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        91
        100.0
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        US-10-351-985-64
        Sequence 63, Appl 200.0

        22
        91
        100.0
        14
        96-09-030-610-72
        Sequence 17, Appl 200.0

        23
        91
        100.0
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        12
        US-10-277-232-72
        Sequence 17, Appl 200.0

        24
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        12
        US-10-277-232-108
        Sequence 108, Appl 200.0

        25
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        US-10-277-233-72
        Sequence 108, Appl 200.0

        26
        91
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        14
        US-10-277-233-12
        Sequence 108, Appl 200.0

        26
        91
        100.0
        14
        US-10-277-233-12
        Sequence 108
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ALIGNMENTS

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US-09-030-619-95

| Sequence 95, Application US/09030619B |
| Patent No. US2002035061A1 |
| APPLICANT: Taylor, Robert No. OMPOSTIONS NO METHODS FOR TREATING |
| TITLE OF INVENTION: WITH ANTIBIOTICS |
| TITLE OF INVENTION: Taylor Office Analogue |
| TITLE OF INVENTION: Cationic Peptide Analogue |
| TYPE: PRT |
| ORGANISM: Artificial Sequence |
| FARTURE: FASTURE: |
| FASTURE: FASTURE: |
| FASTURE: |
| TYPE: PRT |
| OTHER INFORMATION: Cationic Peptide Analogue |
| TYPE: PRT |
| OTHER INCORMATION: Cationic Peptide Analogue |
| TAYLOR OFFICE O
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GENERAL INFORMATION:
APPLICANT: Krieger, Timothy J.
APPLICANT: Krieger, Timothy J.
APPLICANT: Krieger, Timothy J.
APPLICANT: Fraser, Douglas
APPLICANT: Erie, Douglas
APPLICANT: Erie, Douglas
APPLICANT: Erie, Douglas
APPLICANT: Braser, Janet R.
APPLICANT: Manical Ha.
APPLICANT: Manical Ha.
APPLICANT: Manical Ha.
APPLICANT: Monical, Patricia J.
APPLICANT: MONICAL APPLICANTON WITH ANTIBIOTICS
FILE REFERENCE: 660081.406C1
CURRENT APPLICATION WIBER: US/10/277,232
CURRENT PILING DATE: 2022-11-27
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 99
LENGTH: 13
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Sequence 3, Application US/10252773

Sequence 3, Application US/10252773

Publication No. US20030131383A1

GENERAL INFORMATION:

APPLICAMT: EVERETY. NICHOLAS P.

APPLICAMT: LAWRENCE, CHRISTOPHER

APPLICAMT: LAWRENCE, CHRISTOPHER

APPLICAMT: LAWRENCE, CHRISTOPHER

APPLICAMT: DAVIES, MAELOR H.

TITLE OF INVENTION: DEGRADATION

FILE REPREMENCE: INFALINK 3.0003

CURRENT APPLICATION UNDERR: US/10/252,773

CURRENT PILING DATE: 1998-11.02

PRIOR APPLICATION NUMBER: 60/106,373

PRIOR APPLICATION NUMBER: 60/106,573

PRIOR PILING DATE: 1998-11-02

NUMBER OF SEQ ID NOS: 27

SEQ ID NO S: 27

SEQ ID NO S: 27

FRUIT DE OF INVENTION VET. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 91; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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Publication No. US20030211537A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ILKKWPWWPWRRK 13
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                    APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Taylor, Robert
APPLICANT: Fraise, Janet R.
APPLICANT: Fraise, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: West, Michael H.P.
APPLICANT: West, Michael H.P.
TITLE OF INVENTION: INPECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: INPECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: NUMBER: US/09/030,619B
CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILLING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSEQ for Windows Version 3.0
TEMBER OF SEQ ID NOS: 232
SEQ ID NO 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Krieger, Timothy J.
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Praser, Janeth A.
APPLICANT: Praser, Janeth B.
APPLICANT: Bries, Douglas
APPLICANT: West, Michael H.P.
APPLICANT: West, Michael H.P.
APPLICANT: McNicol, Patricia J.
TITLE OF INVENTION: INPECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: MITH ANTIBIOTICS
TITLE OF INVENTION: MITH ANTIBIOTICS
TITLE OF EXCIPANTE: 2002-11-27
CURRENT APPLICATION NUMBER: US/10/277,232
CURRENT APPLICATION NUMBER: US/10/277,232
NUMBER OF SEQ ID NOS: 232
SOOTHARE: FREESE FOR WINDOWS VERSION 3.0
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Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels
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100.0%; Score 91, DB 12,
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THER INFORMATION: Cationic Peptide Analogue
Sequence 99, Application US/09030619B
Patent No. US20020035061A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 95, Application US/10277232 Publication No. US20030211537A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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US-10-277-232-95
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RESULT 6 US-10-229-368-5

RESULT 4 US-10-277-232-99 ; Sequence 99, Application US/10277232

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Pred. No. 0.00013;
Mismatches 0; Indels
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Publication No. US20030148945A1

GENERAL INFORMATION:
APPLICANT: McMicol, Patricia J.
APPLICANT: Paulak, Sonia K.
APPLICANT: Paulak, Sonia K.
APPLICANT: Cameron, Dale
APPLICANT: Camero
                                    APPLICANT: Cameron, Dale
APPLICANT: Cameron, Dale
APPLICANT: Guarna, Maria Marta
TITLE OF INVENTION: ANTIMICROBIAL AND ANTI-INFLAMMATORY
TITLE OF INVENTION: PEPPIDES
FILE REFERENCE: 660081.418
CURRENT APPLICATION NUMBER: US/10/229,368
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 140
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 56
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT PRESENT SEQUENCE PRESENTS: ARTIFICIAL SEQUENCE PRESENTS: OTHER INFORMATION: Indolicidin peptide analogs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Indolicidin peptide analogs
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US-10-229-368-58
; Sequence 58, Application US/10229368
; Publication No. US20030148945A1
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LOCATION: (1) ...(1)

OTHER INFORMATION: D-Isoleucine

US-10-229-368-56
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Best Local Similarity 100.0%;
Matches 13; Conservative 0
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ORGANISM: Artificial Sequence
    Rubinchik, Evelina
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NAMMYKEY: MOD RES
LOCATION: (13)
OTHER INFORMATION: D-Lysine
US-10-229-368-57
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Best Local Similarity 100.
Matches 13; Conservative
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100.0%; Score 91; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels
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100.0%; Score 91; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels
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Publication No. US20030148945A1

GENERAL INPORMATION:
APPLICANT: Malvicol, Patricia J.
APPLICANT: Rubinchik, Evelina
APPLICANT: Rubinchik, Evelina
APPLICANT: Rubinchik, Evelina
APPLICANT: Guarna, Maria Marta
TITLE OF INVENTION: PEPTIDES
TILE REFERENCE: 660081.418
CURRENT PAPLICATION NUMBER: US/10/229,368
CURRENT PILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 140

SEQ ID NO 6:
LENGTH: 13
                                                                                                                 APPLICANT: MCMACALON, Patricia J.
APPLICANT: Pawlak, Sonia K.
APPLICANT: Rubinchk, Evelina
APPLICANT: Rubinchk, Evelina
APPLICANT: Guarna, Maria Marta
APPLICANT: Mart
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US-10-229-368-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Indolicidin peptide analogs
US-10-229-368-5
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Sequence 5, Application US/10229368
Publication No. US20030148945A1
GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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Query Match
100.0%; Score 91; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels
                             APPLICANT: Krieger, Timothy J.
APPLICANT: Krieger, Timothy J.
APPLICANT: Movincol, Patrica J.
APPLICANT: Fraser, Janet R.
TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES AND TITLE OF INVENTION: FORMULATIONS THEREOF
FILE REFERENCE: 660081.417
CURRENT APPLICATION NUMBER: US/10/225,087
CURRENT FILING DATE: 2003-01-10
NUMBER OF SEQ ID NOS: 121
SEQ ID NO 6
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ), OTHER INFORMATION: Indolicidin analog US-10-225-087-52
                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INPORMATION: Indolicidin analog US-10-225-087-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
Publication No. US20030171281A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 91; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels
               APPLICANT: MCMINICOL, Patricia J.
APPLICANT: MCMINICOL, Patricia J.
APPLICANT: Pawlak, Sonia K.
APPLICANT: Pawlak, Sonia K.
APPLICANT: Guarna, Dale
APPLICANT: Guarna, Maria Marta
APPLICANT: Guarna, Maria Marta
TITLE OF INVENTION: ANTIMICROBIAL AND ANTI-INFLAMMATORY
TITLE OF INVENTION: PEPTIDES
FILE REFERENCE: 660081.418
CURRENT APPLICATION NUMBER: US/10/229,368
CURRENT APPLICATION NUMBER: 2002-08-26
NUMBER OF SEQ ID NOS: 140
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO S8
LENGTH: 13
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Krieger, Timothy J.
APPLICANT: Krieger, Timothy J.
APPLICANT: McNicol, Patrica J.
APPLICANT: McNicol, Patrica J.
APPLICANT: Braser, Janet R.
APPLICANT: Praser, Janet R.
APPLICANT: Praser, Janet R.
APPLICANT: Praser, Janet R.
APPLICANT: PRESERVE: PROBULATION: PRESERVE: PRESERVE: CURRENT APPLICANTON NUMBER: US/10/225,087
CURRENT FILING DATE: 2003-01-10
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO SEQ ID NOS: 121
SEQ ID NO SEQ ID NOS: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Indolicidin peptide analogs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Indolicidin analog US-10-225-087-5
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US-10-225-087-5
Sequence 5, Application US/10225087
Publication No. US20030171281A1
GENERAL INFORMATION:
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OTHER INFORMATION: D-Isoleucine
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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LOCATION: (13)...(13)
OTHER INFORMATION: D-Lysine
US-10-229-868-58
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          GENERAL INFORMATION:
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Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels
RESULT 13
US-10-225.087-52
IS-quence 52, Application US/10225087
Sequence 52, Application US/10225087
Publication No. US20030171281A1
GENERAL INFORMATION:
APPLICANT: Krieger, Timothy J.
APPLICANT: Fraser, Janet R.
TITLE OF INVENTION: ANTHREROBIAL CATIONIC PEPTIDES AND TITLE OF INVENTION: PORMULATIONS THEREOF
FILE REPERSENCE: 660081.417
CURRENT APPLICANTON NUMBER: US/10/225,087
CURRENT FILING DATE: 2003-01-10
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 52
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US-10-225-087-53
| Sequence 53, Application US/10225087
| Publication No. US20030171281A1
| GENERAL INFORMATION:
| APPLICANT: Krieger, Timothy J.
| APPLICANT: MCNICOl, Patrica J.
| TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES AND TITLE OF INVENTION: PORMULATIONS THEREOF
| TITLE OF INVENTION: PORMULATIONS THEREOF
| FILE REFERENCE: 660081.417
| CURRENT APPLICATION NUMBER: US/10/225,087
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RESULT 12 US-10-225-087-6 ; Sequence 6, Application US/10225087

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                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-10-225-087-54
i Sequence 54, Application US/1025087
i Sequence 54, Application US/1025087
i Publication No. US20030171281A1
i GENERAL INFORMATION:
i APPLICANT: Krieger; Timothy J.
APPLICANT: Fraser, Janet R.
ITILE OF INVENTION: FORMULATIONS THEREOF
ITILE OF INVENTION: FORMULATIONS THEREOF
ITILE SEPERENCE: 660081.417
CURRENT APPLICATION NUMBER: US/10/225,087
CURRENT FLING DATE: 2003-01-10
NUMBER OF SEQ ID NOS: 121
i SOFTWARE: RESESEQ for Windows Version 4.0
i SEQ ID NO 54
ILINGTH: 13
CURRENT FILING DATE: 2003-01-10
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 53
LENGTH: 13
                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
COTHER INFORMATION: Indolicidin analog
US-10-225-087-53
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Indolicidin analog
US-10-225-087-54
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Search completed: May 4, 2004, 15:35:35 Job time: 37.2895 secs

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4, 2004, 15:08:11; Search time 49.6053 Seconds (without alignments) 74.047 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1586107 seqs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 1 ILKKWPWWPWRRK 13 US-09-444-281-35 Scoring table: Perfect score: Searched: Sequence:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

1586107

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2001s: geneseqp2001s: geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_29Jan04:* geneseqp1990s:* geneseqp2000s:* geneseqp1980s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	m	0	378	σ	195 MBI-11 p	318 Amino ac	4 Amino ac	2	20 Amino ac	ο, ·	ហ	4	4	90	55	m	0.2	23	m	'n	90	54	904 Syntheti	1583 Indolicio	Aay91811 Amino aci
SUMMARIES	ΩI	AWI	AAW71690	AAW66378	AAY24609	AAY94495	AAY91818	AAY91774	AAY91773	AAY91820	AAY91819	AAY92795	ABB81254	ADA00554	ADA00506	ADA00555	ADA00553	ADA00507	ADC73323	ADC98853	ADC98905	ADC98906	ADC98854	ADC98904	AAY24583	AAY91811
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Antimicro Synthetic Indolicid Amino aci	Antimicro Synthetic Indolicid Amino aci	Antimicro Synthetic Antimicro Indolicid	Amino aci Antimicro Synthetic Indolicid	Antimicro Synthetic Indolicid
Ada00546 Adc98896 Aay24582 Aay91806	Ada00541 Adc98891 Aay24580 Aay91804	Add00539 Adc98889 Aaw12877 Aay24615	Aay91833 Ada00578 Adc98935 Aay24572	Ada00547 Ada00547 Adc98897 Aay24573
ADA00546 ADC98896 AAY24582 AAY91806	ADA00541 ADC98891 AAY24580 AAY91804	ADA00539 ADC98889 AAW12877 AAY24615	AAY91833 ADA00578 ADC98935 AAY24572	AAY91812 ADA00547 ADC98897 AAY24573
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1661	6686	86 86 86	98666	9888
222 222 203 203 203 203 203 203 203 203		ነພພພພ 1400 <i>C</i>	₩₩44. ₩₩0日	7 የ 4 tu

ALIGNMENTS

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Bacterial, viral, antitumour, food, preservative, inhibitor, growth, bacterium; yeast, endotoxaemia, sepsis, antibiotic, fungal, antiviral; Candida albicans, sterilant, Salmonella, Yersina, Shigella.
                                                         Antimicrobial cationic peptide CP-11.
              AAW12873 standard; peptide; 13 AA.
                                                                                                                                                                                         Gough M;
                                                                                                                                                                           (UYBR-) UNIV BRITISH COLUMBIA.
                                                                                                                                              96WO-IB000996.
                                                                                                                                                             95US-0002687P.
                                           (first entry)
                                                                                                                                                                                         Falla TJ, Hancock REW,
                                                                                                                  WO9708199-A2.
                                                                                                                                               23-AUG-1996;
                                                                                                                                                             23-AUG-1995;
                                           10-DEC-1997
                                                                                                                                06-MAR-1997.
                                                                                                    Synthetic.
                             AAW12873;
RESULT 1
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WPI; 1997-179179/16.

Cationic peptide(s) having anti-microbial activity - used for the inhibition of bacterial and viral growth, as an antitumour agent, and as a food preservative.

Claim 2; Page 65; 89pp; English.

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Dacteria, combined with activity against the medically important fungus Candida ableians. In addition, the peptides are useful as antitumour agents and/or antiviral agents. The peptides may be used as sterilants or preservatives of materials susceptible to microbial or viral contemination, e.g. in processed foods to inhibit Salmonalla, Yersina and Shigella. The peptides are compact and tend to have a unique polyproline type II extended helix structure that permits them to span the membrane with relatively few amino acids. The peptides possess the ability to work synergistically with antibiotics, and in addition, some of then possess anti-endotoxin activity. N.B. The present sequence represents SEQ ID No:1 in the claims and examples of the specification, but differs slightly from the SEQ ID No:1 in the sequence listing on page 51 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MBILL is a small (mcl.wt. 1879) cationic peptide. DNA encoding MBILL has been incorporated into vector pR2h-B1, in which the replication leader (RIL) sequence of RepA (see also AMA71686) is joined to 2 Hpro peptides (see also AAM71692), to provide a vector for expression of MBILL in host cells. The invention provides controlled replication plasmid vectors (RAMP vectors) comprising a replication origin of a small cryptic plasmid and a gene encoding RepA. The vectors can reach very high levels of plasmid replication, but are not lethal to the host cell, and can be used to direct the high level expression of e.g. cytokines, antigens and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Increasing plasmid copy number in a cell with the repA gene product - and an small cryptic plasmid ori sequence, useful for high level expression of e.g. cytokines, antigens or therapeutic proteins.
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MBII1; cationic peptide; plasmid pKL1; small cryptic plasmid; replication; RepA; vector; RAMP.
                                                                                                                                                                                                                                                                                           Score 91; DB 2; Length 13;
Pred. No. 2.1e-06;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 13; Page 54; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW71690 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cationic peptide MBI11 (MW 1879).
                                                                                                                                                                                                                                                                                               100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-CA000214.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                          1 ILKKWPWWPWRRK 13
                                                                                                                                                                                                                                                                                                                                                                                                             1 ILKKWPWWPWRRK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to direct the high le
therapeutic proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-531571/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burian J, Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BURI/) BURIAN J. (KAYW/) KAY W W.
                                                                                                                                                                                                                                                               Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9841636-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW71690;
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AAW71690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a specifically claimed cationic peptide from the present invention. The present invention describes compositions and methods for treating infection, especially bacterial infections. The compositions and methods use cationic peptides in combination with an antibiotic agent which are then administered to a patient to enhance the activity of the antibiotic agent, to overcome: (a) tolerance, (b) acquired resistance, and (c) inherent resistance. The combinations of antibiotics and cationic peptides can provide synergistic activity against a microorganism that is tolerant, inherently resistant, or has acquired resistance to an antibiotic agent. They can be used for killing e.g. bacteria, fungi, parasites and viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New indolicidin peptide analogues - useful for, e.g. enhancing activity of antibiotic or overcoming tolerance, acquired resistance or inherent resistance of microorganisms.
                                                                                                                                                                                                                                                                                   Indolicidin analogue, resistance, cationic peptide, antibiotic;
bacterial infection; tolerance, antibacterial; microorganism; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                 Gaps
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   Length 13;
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
Score 91; DB 2; I
Pred. No. 2.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 91; DB 2; I
Pred. No. 2.1e-06;
; Mismatches 0;
                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser JR, West MHP, Mcnicol PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; Page 93; 105pp; English.
                                                                                                                                                                 AAW66378 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                        Cationic peptide of claim 15 #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MICR-) MICROLOGIX BIOTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0040649P.
97US-00915314.
97US-0060099P.
98US-00030619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.08;
 Query Match
Best Local Similarity 100.0%;
Matches 13; Conservative 0
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Best Local Similarity 100.0%;
Marches 13; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-CA000190
                                                                                                                                                                                                                          12-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ILKKWPWWPWRRK 13
                                                                                1 ILKKWPWWPWRRK 13
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                                                                                                                                                                                                                                                                                                                  fungus; parasite; virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13 AA;
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26-SEP-1997;
25-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                         17-SEP-1998
                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                               AAW66378;
                                                                                                                                    RESULT 3
                                                                                                                                                   AAW66378
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RESULT 4

Sequence 13 AA

Cellulose binding domain; CBD; cationic peptide; MBI-11; indolicidin; bovine.

MBI-11 peptide derived from indolicidin.

(first entry)

20-SEP-2000

AAY94495;

AAY94495 standard; peptide; 13 AA.

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AAY24549 to AAY24615 represent indolicidin analogues of formulae (I)-
(VIII) containing up to 25 amino acids (aa): RXZXXZXB (I), BXZXXZXB (II),
BBBXZXXXXB (III), BXZXXZXBBB(AA) MILIBBAGS (IV), BXZXXZXBB (AA) MM (V),
LBBDXZMXZXZXKK (VII), LKNZXXZXXRK (VII) and BRXZXXZXBB (AIII). Where Z
COFK, AA = any aa, n = 0 or 1; in (II), at least 1 Z = V; in (VIII) at
least 2 X = F or Y. The analogues are used to treat infections caused by
bacteria (Gram positive or negative, or anaerobic); fungi (yeast or
moulds); parasites (protozoa, nematodes, cestodes or trematodes) or
viruses. Typical of very many pathogens, that can be controlled are
Leishmania, Trypanosoma, Ascaris lumbricoides, Fasciola hepatica,
Klebsiella pneumoniae, Bordetella pertussis, Staphylococcus aureus,
Listeria, Clostridium, rotavirus and papilloma virus. Compounds derived
from the analogues may be used seinilarly; the compounds may also be
prepared from antibiotics or antiarrythmic agents. The analogues may be
used therapeutically or to coat medical and expense.
Cor herbicides, or as preservatives for foods and technical materials. The
analogues are administered by injection, lavage, orally or topically,
generally at 0.1-50 mg/kg. These analogues have a broader spectrum of
activity than indolicidin and modification as compounds reduces their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New indolicidin analogues with antimicrobial activity and related nucleic acid - vectors, transformed cells and antibodies, also conjugates with polyoxyalkylene glycol and fatty acid to reduce toxicity, useful therapeutically, as disinfectants etc.
                                                                                                                                                                   Indolicidin; bacterial infection; photo-oxidised solubiliser; antihicrobial; antibiotic; antiarrythmic; surface disinfectant; additive; shampor; soap; insecticide; herbicide; preservative; food; technical material.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 91; DB 2; Length 13
100.0%; Pred. No. 2.1e-06;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Erfle D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Taylor R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 32; 129pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fraser JR, West MH, Krieger TJ,
                    AAY24609 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MICR-) MICROLOGIX BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0024754P.
97US-0034949P.
                                                                                                                                                                                                                                                                                                                                                                                 97WO-US014779
                                                                                            (first entry)
                                                                                                                                 Indolicidin analogue #61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-169090/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13 AA;
                                                                                                                                                                                                                                                                                                         WO9807745-A2
                                                                                                                                                                                                                                                                                                                                                                                                                      21-AUG-1996;
13-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                 21-AUG-1997;
                                                                                               18-AUG-1999
                                                                                                                                                                                                                                                                                                                                           26-FEB-1998
                                                                                                                                                                                                                                                                    Synthetic.
                                                          AAY24609;
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AAY24609
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Cationic peptide; tumour; pharmaceutical composition; cancer; treatment; leukaemia; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma; breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon;
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                     .
                                                                                                                                                                                                                                                                                                                       Length 13;
                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of cationic peptide MBI 11E1CN.
                                                                                                                                                                                                                                                                                                                      100.0%; Score 91; DB 3; L
100.0%; Pred. No. 2.1e-06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                 AAY91818 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                   1 ILKKWPWWPWRRK 13
                                                                                                                                                                                                                                                                                                                                                               1 ILKKWPWWPWRRK 13
                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           multidrug resistance.
                                                                                                                                                                                                                                                                                                          Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                               AAY91818;
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
AAY91818
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Gaps ·.

> 1 ILKKWPWWPWRRK 13 1 ILKKWPWWPWRRK 13 Conservative

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RESULT 5

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A novel method allows the efficient production of cationic peptides in recombinant host cells. The method involves construction of a multidomain fusion protein expression cassette comprising a promoter and a nucleic acid molecule expressed as an insoluble protein. The inclusion of anionic peptide sequences in the linker sequences neutralises the positive charge of the cationic peptide so that the charge of the fusion of the cationic peptides to that the charge of the fusion of the cationic peptides such as bovine indolician may be used as antimicrobial agents. The present sequence is the MBI-11 peptide. MBI-11 is a cationic peptide derived from modifications of

indolicidin

Multi-domain fusion protein expression cassette used for high yield stable production of foreign peptide gene products.

MICR-) MICROLOGIX BIOTECH INC.

Bartfeld D;

Burian J,

WPI; 2000-400086/34.

98US-0109218P.

20-NOV-1998; 19-NOV-1999;

WO200031279-A2.

Bos taurus.

02-JUN-2000.

Disclosure; Page 24; 73pp; English.

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Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                   AAY91773;
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                                                                                                                                                                                                                                            RESULT 8
                                                                                                                                                                                                                                                     AAY9177
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                                                                                                                                                                                     This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxyalkylene (APO) modified cationic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with a multidrug resistant phenovype. The pharmaceutical composition can be used to treat tumours, specifically lymphoma, leuksemia, multiple myeloma, or tumours of breast, lung, ovary, cervix, uterus, skin, prostate, liver and colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cationic peptide; tumour; pharmaceutical composition; cancer; treatment; leukaemia; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma; breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel pharmaceutical composition containing optionally activated polyoxyalkylene-modified cationic peptides, useful for treating tumors.
                                                                                                                                          Novel pharmaceutical composition containing optionally activated polyoxyalkylene-modified cationic peptides, useful for treating tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       West MHP;
                                                                                                   West MHP;
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fraser JR,
                                                                                                   Fraser JR,
                                                                                                                                                                                                                                                                                                                 Score 91; DB 3; Length 13;
Pred. No. 2.1e-06;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of cationic peptide MBI 11CN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Krieger TJ, Taylor R, Erfle D,
                                                                                                   Erfle D,
                                                                                                   Taylor R,
                                                                                                                                                                        Disclosure; Page 15; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                AAY91774 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                (MICR-) MICROLOGIX BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MICR-) MICROLOGIX BIOTECH INC
                                                                                                                                                                                                                                                                                                                  100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-00096541.
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                                                            98US-00096541.
                                        99WO-CA000552
                                                                                                    Krieger TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                           1 ILKKWPWWPWRRK 13
                                                                                                                                                                                                                                                                                                                                                                              ILKKWPWWPWRRK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     breast; lung; ovary;
multidrug resistance.
                                                                                                                       WPI; 2000-223549/19.
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Friedland HD,
                                                                                                    Friedland HD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09965506-A2
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  WO9965506-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUN-2000
                                         14-JUN-1999;
                                                            12-JUN-1998;
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                     23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxyalkylene (APO)-modified cationic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with a multidrug resistent phenotype. The pharmaceutical composition can be used to treat tumours, specifically lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary, cervix, uterus, skin, prostate, liver and colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                               This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxyalkylene (APO)-modified cationic peptide. The modification of peptides with APO increases their activity against tumour pharmaceutical composition am unlidiary resistent phenotype. The pharmaceutical composition can be used to treat tumours, specifically lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary, cervix, uterus, skin, prostate, liver and colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cationic peptide; tumour; pharmaceutical composition; cancer; treatment; leukaemia; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma; breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            West MHP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 91; DB 3; L
100.0%; Pred. No. 2.1e-06;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of cationic peptide MBI 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 14; 94pp; English.
Example 3; Page 14; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY91773 standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MICR-) MICROLOGIX BIOTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ILKKWPWWPWRRK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ILKKWPWWPWRRK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  multidrug resistance.
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Friedland HD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JUN-1999;
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Length 13;

DB 3;

100.0%; Score 91;

us-09-444-281-35.rag

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Amino acid sequence of cationic peptide MBI 11E2CN
                                                                                                                                                                                                Krieger TJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                            13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                Friedland HD,
                                                                                                                                      14-JUN-1999;
                                                                                                                                                         12-JUN-1998;
                                                                                               W09965506-A2
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02-NOV-1998;
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                                                                                                                  23-DEC-1999.
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                                                                             Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxyalkylene (APO)-modified cationic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with a multidrug resistant phenotype. The pharmaceutical composition can be used to treat tumours, specifically lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary, cervix, uterus, skin, prostate, liver and colon
                                                                                                                                                                                     Cationic peptide; tumour; pharmaceutical composition; cancer; treatment; leukaemia; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma; breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon; multidrug resistance.
                                                                                                                                                                                                                                                                                                                                                                                               Novel pharmaceutical composition containing optionally activated polyoxyalkylene-modified cationic peptides, useful for treating tumors
                                                                                                                                                                                                                                                                                                                                                         West MHP;
                   Gaps
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                                                                                                                                                                                                                                                                                                                                                         Fraser JR,
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                   0; Indels
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                                                                                                                                                                  Amino acid sequence of cationic peptide MBI 11E3CN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 91; DB 3; I 100.0%; Pred. No. 2.1e-06;
         Pred. No. 2.1e-06;
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                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                         AAY91820 standard; peptide; 13 AA.
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100.08; Fr.
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                                                                                                                                                                                                                                                                                                                                     (MICR-) MICROLOGIX BIOTECH INC.
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                                                                                                                                                                                                                                                                                                                                                         Friedland HD, Krieger TJ,
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                                                                                                                                                 (first entry)
                                                        13
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Best Local Similarity 100.
                                     1 ILKKWPWWPWRRK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ILKKWPWWPWRRK 13
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                   Conservative
                                                        1 ILKKWPWWPWRRK
                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-223549/19.
         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13 AA;
                                                                                                                                                                                                                                                          WO9965506-A2
                                                                                                                                                                                                                                                                                                14-JUN-1999;
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                   13;
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                                                                                                                             AAY91820;
                   Matches
                                                                                              AAY91819
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This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxyalxylene (APO)-modified cationic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with a multidrug resistant phenotype. The pharmaceutical composition can be used to treat tumours, specifically lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary, cervix, uterus, skin, prostate, liver and colon
Cationic peptide; tumour; pharmaceutical composition; cancer; treatment; bridkeemis; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma; breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon; multidrug resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel pharmaceutical composition containing optionally activated polyoxyalkylene-modified cationic peptides, useful for treating tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Magainin, antimicrobial, transgenic plant; protease degradation; Rev4; indolicidin; protein production; reverse peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        West MHP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Taylor R, Erfle D, Fraser JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 91; DB 3; Length 13
100.0%; Pred. No. 2.1e-06;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 15; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY92795 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MICR-) MICROLOGIX BIOTECH INC.
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The present invention describes an antibacterial compound (1), comprising a conjugates of glycopeptide and peptidic membrane-associating elements.

(1) comprises the formula VL-W-X, where: V = a glycopeptide molety that inhibits peptidoglycan biosynthesis in bacteria; L = a linking group; W = c a peptidic membrane-associating element; and X = H or a membrane-c insertive element. Also described: (1) a method of treating or preventing configuration comprising the administration of (1); and (2) use of a bacterial infection. (1) are used in the manufacture of a medicament or prophylaxis of a bacterial infection in a human or configural body, including both the gram positive and gram negative bacteria including Mycobacterium Sp., Buterococcus Sp., Borrelia Sp., Actinomyces Sp., Hemophilus Sp., Clostridium Sp., Berteriolaria Sp., Actinomyces Sp., Hemophilus Sp., Clostridium Sp., Perdomonas Sp., Actinomyces Sp., Pervent adhesion of bacterial confirms provide the available of prophylaxis. (1) are also useful as wound treatment agents to metrix proteins, especially fibrosectin, prevent adhesion of bacterial confirms proteins associated biosynthetic proteins. Consuming the hospholipids than the eukaryotic organisms, also having a higher proportion of acidic phospholipids than the eukaryotic organisms, also with (1) and is effective to treat the antibiotic resistant bacterial communistical pages of the present invaries in peptides given in the communistical pages of the present invaries of the present invaries.
                         Antibacterial compound, useful for the treatment of a bacterial infection by e.g. gram positive or negative bacteria, comprises a conjugate of glycopeptide and peptidic membrane-associating element.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antimicrobial; cationic; viscosity-increasing agent; solvent; buffer; antibacterial; virucide; antiinflammatory; fungicide; protozoacide; parasticides, vulnorary; dermatological; herbicide; insecticide; infection; systemic infection; sepsis; acne; disinfectant; herbicide; insecticide; silicone sealant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 91; DB 5; Length 13; larity 100.0%; Pred. No. 2.1e-06; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial cationic peptide 11E2CN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                              Disclosure; Page 21; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADA00554 standard; peptide; 13 AA.
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA00554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
ADA00554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          원
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                Indolicidin is a potent antimicrobial tridecapeptide, originally purified from cytoplasmic granules of bovine neutrophils. CP-11 is an analogue, which has better activity against E coli Pseudomonas aeruginosa and candida albicans, but reduced activity against Staphylococcus aurents. reverse peptide, Rev4 (AAY22796) of indolicidin was found to have increased teability against plant proteases degradation. Expression of antimicrobial peptides in transgenic plants suffers a major limitation in that the foreign peptides are susceptible to rapid degradation by proteases. The invention concerns reducing the extent of protease degradation of a protein applied to, or produced by a plant by administering indolicidin, Rev4 or a functional equivalent to the plant. Transgenic plants expressing indolicidin and Rev4 are useful for production of the antimicrobial peptides. Compositions containing indolicidin and Rev4 are useful for indolicidin and Rev4 are useful for indolicidin and Rev4 are useful for production of agronomically indolicidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibacterial; glycopeptide; peptidic membrane associating element; bacterial infection; vancomycin; peptidoglycan biosynthesis inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                               Polypeptides for reducing proteolytic degradation of proteins administered to, or produced by a plant comprise indolicin or its functional equivalents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 91; DB 3; Length 13; 100.0%; Pred. No. 2.1e-06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CP11-NH2 antibacterial peptide SEQ ID NO:21.
                                                            Davies MH
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(INTE-) INTERLINK BIOTECHNOLOGIES LLC. (KENT ) UNIV KENTUCKY RES FOUND.
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                                                          Lawrence C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-NOV-2000; 2000GB-00026924.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         important proteins in plants
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Matches 13, Conservative
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                                                                                              WPI; 2000-365597/31
                                                            Ľį Ö,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13 AA;
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                                                            Everett NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibiotic.
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The present invention describes a composition (A) comprising an antimicrobial cationic peptide (I), a viscosity-increasing agent (II) and antimicrobial cationic peptide (I), a viscosity-increasing agent (III) and cationic peptide (II) acomposition comprising (I), buffer (IV) and (III). (I) has antibacterial, vincide, antihifiammatory, fungicide, protozoacide, parasiticide, vulnerary, dermatological, computation of microflora (eukaryotes, prokaryotes or viruses) at a target of population of microflora (eukaryotes, prokaryotes or viruses) at a target site, particularly for treatment or prevention of infections. They can be used to creat a wide range of systemic infections (e.g. sepsis) and for cosed to reat medical devices have been, or will be, inserted into the body (alternatively, they are used to treat the devices); and (ii) at sites on the skin (particularly for treating acno) or the mucosa. The devices treated are especially central venous, vascular dialysis, pulmonary created are especially for treatment of clothing and air filters; in cosmetics and soaps; as herbicides and insecticides; in building compariate (e.g. siliceone sealants) and in processing animal products, e.g. bides. The present sequence represents an antimicrobial actionic peptide, which is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 91; DB 6; Length 12. Pred, No. 2.1e-06;
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                                                              (MICR-) MICROLOGIX BIOTECH INC.
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20-AUG-2002; 2002US-00225087.
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Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                               Mcnicol PJ,
                                                                                                                                                                                             WPI; 2003-332767/31.
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                                                                                                                                   Krieger TJ,
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ADA00555
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                                                                                                                                                                                             Fraser JR;
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                                                                                                                        (MICR-) MICROLOGIX BIOTECH INC
                           21-AUG-2001; 2001US-0314232P.
20-AUG-2002; 2002US-00225087.
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                                                                                                                                                                                             ЪД,
                                                                                                                                                                                          Mcnicol
                                                                                                                                                                                                                                                     WPI; 2003-332767/31
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(MICR-) MICROLOGIX BIOTECH INC. 21-AUG-2001; 2001US-0314232P. 20-AUG-2002; 2002US-00225087.

Mcnicol PJ, Fraser JR; Krieger IJ,

Composition containing stabilized antimicrobial cationic protein, useful for treating infections, particularly where associated with in-dwelling WPI; 2003-332767/31.

Claim 47; Page 48; 90pp; English.

devices.

The present invention describes a composition (A) comprising an antimicrobial cationic peptide (I), a viscosity-increasing agent (II) and a solvent (III). Also described is a composition comprising (I), buffer (IV) and (III). (I) has antibacterial, virucide, antiinflammatory, the antibacterial, virucide, antiinflammatory, fungicide, protozoacide, parastricide, vulnerary, dermatological, persistence, parastricide, vulnerary, dermatological, perplaid of microfica activities, (A) can be used to read a target site, particularly for treatment or prevention of infections. They can be set to treat a wide range of systemic infections (e.g. sepsis) and for topical treatment of wounds, but most especially can be used; (i) at sites where medical devices have been, or will be, inserted into the body caterntively, they are used to treat the devices) and (ii) at sites on the skin (particularly for treating acne) or the mucosa. They devices treated are especially central venous, vascular dialysis, pulmonary are treaty. peritomeal adialysis or umbilical catheters. They may also be used as surface disinfectants; for treatment of clothing and air filters; in cosmetics and soaps; as herbicides and insecticides; in building community and present sequence represents an antimicrobial cationic error peptide, which is used in the exemplification of the present invention.

Sequence 13 AA;

0; Gaps Query Match
Best Local Similarity 100.0%; Pred. No. 2.16-06;
Matches 13; Conservative 0; Mismatches 0; Indels

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ઠે d Search completed: May 4, 2004, 15:19:39 Job time: 50.6053 secs

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Q80vt9 mus musculu Q80vt9 mus musculu Q9pe93 xanthomonas Q9dc80 tt virus. O Q9tg4 desulfitoba Q9bb1 xanthomonas Q9bb4 homo sapien Q94712 porcine epi Q84712 porcine epi Q84712 porcine epi Q84712 porcine epi Q8471 homo sapien Q9441 homo sapien Q9441 homo sapien Q94476 drosophila Q8446 methanopyru
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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QBRP93
Q9DUC4
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Q9DT81
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Q8gzx7 oryza sat1v	Q8GZX7	10	198	ö	•	45
rosophila	Q9Y0E8	S	157	50.0	49.5	44
~	Q9JH31	12	746	ö	20	
	075035	4	466	ö	50	
Q92vq2 rhizobium m	Q92VQ2	16	337	ö	50	41
	Q7XFD1	10	327	ö	50	
13 oryza	Q9AUN3	10	327	ö	50	
oryza	Q84ST7	10	137	ö	20	
therm	Q9WYF1	16	83	ó	50	
Q8seb4 elaenia fal	Q8SEB4	ω	55	ö	50	
7	Q91HP7	12	988	ä	ċ	
Q9yw19 melanoplus	Q9YW19	12	970	Ξ.	50.5	
Q9n9t4 leishmania	Q9N9T4	ß	214	۲.	ö	33
Q8yy85 anabaena sp	QSYY85	16	689	ä	51	
Q13161 homo sapien	Q13161	4	530	ä	51	
٠.	Q7V805	16	403	ä	51	
	Q8ZU59	17	298	ä	51	29
Q9b6t0 eudromia el	Q9B6T0	80	55	ä	. 51	
2 strepto	QB2HM2	16	350	ζ.	51.5	
Q7vi01 helicobacte	Q7VI01	16	388	ď	52	
Osdjh5 synechococc	QBDJHS	16	351	ď	52	
	Q88HH3	16	282	ď	52	
Q8ppu5 xanthomonas	QBPPUS	16	105	ď	52	
Q8p4z9 xanthomonas	Q8P4Z9	16	102	ď	52	
Q934j3 prevotella	Q934J3	7	640	ω.	52.5	
Q9y7v5 trichoderma	Q9Y7V5	ĸ	1245	۳.	53	
rosophi	QBIGB8	Ŋ	9	m.	53	
O92380 bombyx mori	092380	12	331	'n	53	
rachipl	Q8B9N6	12	328	53.5	53	17

ALIGNMENTS

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STRAIN=FVB; TISSUE=Scapular skin;
MEDLINE=21185977; PubMed=11290294;
Tkatchenko A.V., Visconti R.P., Shang L., Papenbrock T., Pruett N.D.,
Ito T., Ogawa M., Awgulewitsch A.;
"Overexpression of Hoxol3 in differentiating keratinocytes results in
downregulation of a novel hair keratin gene cluster and alopecia.";
Development 128:1547-1558(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090,
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Pred. No. 0.6;
0, Mismatches 2; Indels
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SECUENCE FROM N.A.
STRAIN=FVB; TISSUE-Scapular skin;
TKAtchenko A.V., Pruett N.D., Awgulewitsch A.;
Submitted (ANN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF477980; AAO33770.1; -.
NOW TER
SEQUENCE 83 AA; 10834 MW; F7BB37E12A327BCD CRC64;
                                                                                                                                                                                01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Krtaple.10 (Fragment).
Mus musculus (Mouse)
                                                                                          83 AA
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Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                          PRELIMINARY;
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SEQUENCE FROM N.A.
                                                                                          QB0VT9
RESULT 1
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PWLWPWWLW 31

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EMBL; AB041959; BAB19313.1;
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Matches
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SEQUENCE FROM N.A.

SEQUENCE TRAIN=ATCC 33913 / NCPPB 528;

XX MEDILNE=2202145; PubMed=12024217;

XX da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciaphna L.P.,

RA Carelli R.M.B., Coulinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Fatsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.R.,

Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Actiss E.C., Machadanis J., Menck C.F.M., Miyaki C.Y., Mono D.H.,

Moreira L.M., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Tarkita M.A., Tamura R.E., Telxeira B.C., Tezza R.I.D.,

Spinola L.A.F., Tarkita M.A., Tamura R.E., Telxeira B.C., Tezza R.I.D.,

A Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

A Secubal J.C., Kitajima J.F.,

Locaparison of the genomes of two Xanthomonas pathogens with differing
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                                                                                                                                                                                                                                                                                                        Bacteria; Protechacteria; Gammaprotechacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas.
NCBI_TaxID=340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.6%; Score 59; DB 16; Length 780; 75.0%; Pred. No. 17; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Okamoto H.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AE012102; AAM39407.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 780 AA; 85074 MW; 12867434D1852549 CRC64;
                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein XCC0088.
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NCBL_TaxID=68887;
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                                                                  780 AA
                                                                                                                                                                                                                                                                                    Xanthomonas campestris (pv. campestris)
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                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 417:459-463 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 WPWHWWPW 155
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Mf-TTV9;
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TT virus.
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                                                                  QBPE93
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Matches
   RESULT 2
Q8PE93
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Davis J.K., Tiedje J.M.;
Davis J.K., Tiedje J.M.;
Sequence and transcriptional analysis of reductive dehalogenase genes
"Sequence and transcriptional submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR403185; AAL87800.1; -.
InterPro; IPR006311; Tat.
TIGRFAMS; TIGR01409; TAT_signal_seq; 1.
                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mypothetical protein.
Desulfitobacterium hafniense.
Bacteria; Firmicutes; Clostridia; Clostridiales; Peptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Okamoto H., Nishizawa T., Tawara A., Takahashi M., Kishimoto J.,
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                                                                                                                                                                                                      57.6%; Score 57; DB 12; Length 723; 100.0%; Pred. No. 27; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.6%; Score 55; DB 12; Length 49; 44.4%; Pred. No. 4.4; 1; Mismatches 3; Indels
GO, GO:0004185; F:serine Carboxypeptidase activity; IEN GO; GO:0006508; P:proteclysis and peptidolysis; IEA. InterPro; IPR001563; Peptidase Slo.
InterPro; IPR004219; TTvirus_Unk.
Pfam; PF02556; TT ORF1; 1.
PROSTIE; PS0131; 1.
SEQUENCE 723 AA; 85393 MW; 232D003099766344 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 49 AA; 7225 MW; 1DA6F8F1AB69AA43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TT virus.
Viruses; ssDNA viruses; Circoviridae; Anellovirus.
NCBI_TaxID=68887;
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EMBL; AB050449; BAB19930.1; -.
NON TER 49 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 AA.
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MEDLINE=20568739; PubMed=11118348;
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 7; Conservative
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nes 8; Conserv
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Gaps

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RESULT 6

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Q8PBI7

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Okamoto H., Nishizawa T., Tawara A., Takahashi M., Kishimoto J.,
Sai T., Sugai Y.,
"TT virus mRNAs detected in the bone marrow cells from an infected
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Pred. No. 48;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21488921; PubMed=11601907;
Okamoto H., Nishizawa T., Takahashi M., Asabe S., Tsuda F.,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                       SEQUENCE FROM N.A.
TISSUES-Kin, and amelanotic;
Strausberg N.,
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC015687, AAH15687.1; -.
Hypothetical protein.
SEQUENCE 342 AA, 37741 MW; 3147596F8D7DF849 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88552 MW; D65CCB2CAA5CE26F CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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NCBI_TaxID=68897;
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EMBL; AB050448; BAB1928.1; -.
InterPro. IPR004219; TTvirus Unk.
Pfan; PC2955; TT 08E1; 1.
SEQUENCE 748 AA; 88552 MW; D65CCB2CAA5CE26F (
                                                                                                                                                                                                                                                                                                                                             Score 55; DB 4;
Pred. No. 24;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 750 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20568739; PubMed=11118348;
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                                                                                                                                                                                                                                                                                                                                                    55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 63.0
Tr Conservative
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                       NCBI_TaxID=9606;
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SEQUENCE FROM N.A.

STRAIN-ATCC 33913 / NCPPB 528;

MEDINE-2202145; PubMed=12024217;

MADINE-2202145; PubMed=12024217;

MA Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A da Silva A.C.R., Forno J.A., Berchlini M.C., Camargo L.B.A.,

A laves L.M.C., do Amaral A.M., Bercolini M.C., Camargo L.B.A.,

Camarcte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

A cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., Ciapina L.P.,

Raria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Formighieri B.F., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.P.,

Ratius B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins B.C., Machado M.A., Manck C.F.M., Miyaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira W.R.,

Spinola L.A.P., Takita M.A., Tamura R.B., Teixeira B.C., Tezza R.I.D.,

Spinola L.A.P., Takita M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D.,

Standade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Setubal J.C., Kitajima J.P.;

Comparison Of the genomes of two Xanthomonas pathogens with differing
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GO; GO:0009002; F:serine-type D-Ala-D-Ala carboxypeptidase ac. .; IEA.
InterPro; IRR003709; Pept_MISB_MISC.
Pfam; PF02557; VanY; Pept_MISB_MISC.
Hypothetical protein; Complete protecme.
SEQUENCE 208 AA; 22940 MW; 10B180F6EAF7B014 CRC64;
                                                                                                                                                           Gaps
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypotherical protein.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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Bacteria, Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadacee; Xanthomonas.
NCBI_TaxID=340;
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                                                                                           Ouery Match 55.6%; Score 55; DB 2; Length 152; Best Local Similarity 85.7%; Pred. No. 12; Matches 6; Conservative 0; Mismatches 1; Indels
Hypothetical protein.
SEQUENCE 152 AA; 16876 MW; 2F5A00F01E70A379 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QBPBI7;
01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein XCC1132.
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Nature 417:459-463(2002).
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Gaps

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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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EMBL, 225:483; CAR80971.1; -...
InterPro; IPR002551; Corona_S1.
InterPro; IPR002552; Corona_S2.
Pfam; PF01601; Corona_S1; 1.
CONFLICT 422 422 Y -> N (IN REP. 1).
                                                                                                                                                     Gaps
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Pordine epidemic diarrhea virus (strain Br1/87) (PEDV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
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Duarte M., Laude H.;
"Sequence of the spike protein of the porcine epidemic diarrhoea
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MEDIJNE=93389433; PubMed=8397280;
MEDIJNE=93389433; PubMed=8397280;
Bridgen A., Duarte M., Tobler K., Laude H., Ackermann M.;
Sequence determination of the nucleocapsid protein gene of the porcine epidemic diarrhoea virus confirms that this virus is a coronavirus related to human coronavirus 292 and porcine transmissible gastroenteritis virus.";
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MEDLINE=94120721; PubMed=8291230;
Duarte M., Tobler K., Bridgen A., Rasschaert D., Ackermann M.,
Laude H.;
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                                                                                                        Length 750;
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741C84D5DD3BDC4D CRC64;
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                                                         89223 MW; 616EC86DC3469091 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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85.7%; Pred. No. 1.1e+02;
ive 0; Mismatches 1;
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Last sequence update)
                                                                                                        Score 55; DB 12;
Pred. No. 48;
1; Mismatches 3.
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                      InterPro; IPR004219; TTvirus_Unk. Pfam; PF02956; TT_ORF1; 1. SEQUENCE 750 AA; 89223 MW; 61.
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                                                                                                          Ouery Match
Best Local Similarity 44.4%;
Matches 8; Conservative
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Q91AV1,
01-DEC-2001 (TYEMBLYEL: 19,
01-DEC-2001 (TYEMBLYEL: 19,
      EMBL; AB060592; BAB69900.1;
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Matches 6; Conserv
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"Sequence analysis of the porcine epidemic diarrhea virus genome
between the nucleocapsid and spike protein genes reveals a polymorphic
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Bridgen A., Kocherhans R., Tobler K., Carvajal A., Ackermann M.;
"Further analysis of the genome of porcine epidemic diarrhea virus.";
Adv. Exp. Med. Biol. 440:781-786 (1998).
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01-MAR.2003 (TIEMBLIE). 23, Last sequence update)
01-MAR.2003 (TIEMBLIE). 24, Last annotation update)
Spike protein.
Spike protein.
Spike protein.
Viruses, ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
Spike protein.

Porcine epidemic diarrhea virus (strain CV777) (PEDV).

Viruses, ssRNA positive-strand viruses, no DNA stage; Nidovirales;

Coronaviridae, Coronavirus.
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Duarte M., Tobler K., Bridgen A., Rasschaert D., Ackermann M.,
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                                                                                                                                                                  MEDIJNE=93389433; PubMed=8397280; BEGUENCE FROM N.A. Bridgen A., Duarte M., Tobler K., Laude H., Ackermann M.; Bridgen A., Duarte M., Tobler K., Laude H., Ackermann M.; Berguence determination of the nucleocapsid protein gene of porcine epidemic diarrhea virus confirms that this virus is coronavirus related to human coronavirus 229E and porcine transmissible gastroenteriis virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kocherhans R., Bridgen A., Ackermann M., Tobler K.; "The complete genome sequence of porcine epidemic diarrhea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AFF35311, AAK38656.1, -...
InterPro; IPR002551; Corona_S1.
InterPro; IPR02552; Corona_S2.
Pfam; PF01601; Corona_S1, 1...
Pfam; PF01601; Corona_S2, 1...
SEQUENCE 1393 AA, 151552 MW; 022E5E5E5435876D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=96112302; PubMed=8830538;
Tobler K., Ackermann M.;
TEDLY leader sequence and junction sites.";
Adv. Exp. Med. Biol. 380:541-542(1995).
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Best Local Similarity 85.,
6; Conservative
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SEQUENCE FROM N.A.
STRAIN=Chinju99;
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PIR, T12505, T12505.
Hypothetical protein.
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SEQUENCE 299 AA, 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Berkeley;
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                                                                                                                                                                                                                                                                                                      RESULT 15
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Kang T.-J., Lim Y.-Y., Jang Y.-S., Kwon T.-H., Kim D.-H., Yang M.-S.;

Kang T.-J., Lim Y.-Y., Jang Y.-S., Kwon T.-H., Kim D.-H., Yang M.-S.;

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AFS00215, AAM19716.11, -1.

InterPro; IPR002551; Corona S1.

InterPro; IPR002552; Corona S1.

Ffam; PF01600, Corona S1: 1.

Pfam; PF01601; Corona S1: 1.

SEQUENCE 1386 AA; IS1853 MW; IIF98BCB2AA0526B CRC64;
                                                                                                                                                                                                                                                                                    Gaps
Yeo S.-G., Krell P., Nagy E.;
"Cloning and nucleotide sequence analysis of spike gene of porcine publicant diarrhea virus detected in Korea.";
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX16785; AAN86621.1; -.
InterPro; IPR00255; Corona.S1.
InterPro; IPR02552; Corona.S2.
Pfam; PF01609; Corona.S1: 1.
Pfam; PF01601; Corona.S1: 1.
Pfam; PF01601; Corona.S1: 1.
SEQUENCE 1383 AA; 151582 MW; BSBA4D7EB5371A54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porcine epidemic diarrhea virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
NCBL_TaxID=28295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Testis;
Ansorge W., Wirkner U., Mewes H.W., Gassenhuber J., Wiemann S.;
Submitted (UNT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO96/T53; CAB46428.2; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
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                                                                                                                                                                                                                                     54.5%; Score 54; DB 12; Length 1383; 85.7%; Pred. No. 1.1e+02; ive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1386;
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Pred. No. 1.18+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein (Fragment)
DKFZP434C192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1386 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.5%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                  1322 KWPWWW 1328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                            5 KWPWWPW 11
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spike protein.
                                                                                                                                                                                                                                          Query Match
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Q8QQ98;
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Q8QQ98
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PROPRETED PROCESS.

WHY DEPRETED PROCESS.

DOSTORED 299 AN; 3102 MM; ERROBEORGEARRESSS ACC64;

DOSTORED S.

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2; Indels 0; Gaps
Query Match
Best Local Similarity 77.8%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 2; Indels
                                                                     2 LPWKWPWWP 10
||||| | |
62 LPWKWAWLP 70
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Search completed: May 4, 2004, 15:22:11 Job time : 35.886 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 4, 2004, 15:15:37; Search time 11.9737 Seconds (without alignments) 104.437 Million cell updates/sec

US-09-444-281-35 91 1 ILKKWPWWPWRRK 13 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 Total number of hits satisfying chosen parameters:

283366 segs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Ğ	E2 glycoprotein pr	pr	hypothetical prote	~	ADP r		>4	myosin heavy chain	hypothetical prote	Ω,	hypothetical prote	NADH oxidase (H2O2	hypothetical prote	histidinol-phospha	peplomeric polypro	peplomeric polypro	E2 glycoprotein pr	glycoprotein	glycoprotein		ycoprotei	r of dru	prot	ical prot		prot	nctional bi	probable short-cha
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SUMMARIES	ΩI	JC1222	VGIHHC	T12505	B72492	E89605	JT0751	833068	B70741	A59287	T29295	AH0755	T36208	S23449	G70715	S77354	S37664	S37663	VGIHIB	VGIHAK	S07421	S14939	S14940	S55483	T22175	T22177	565812	AC1954	F82646	B83161
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probable membrane	hypothetical prote	anthranilate synth	probable membrane	probable membrane	probable mmpL4 pro	probable mmpL2 pro	cyclic-nucleotide	E2 glycoprotein pr	E2 glycoprotein -	E2 glycoprotein pr	E2 glycoprotein pr	E2 glycoprotein pr	surface protein -	surface glycoprote	E2 glycoprotein pr
B70763	H72376	A39128	819439	E70826	C70831	F70746	A48508	S24284	A36607	VGIHMU	VGIH59	JQ2168	829998	A37474	VGIHINM
N	N	~	N	0	N	N	N	н	N	Н	Н	Н	N	7	н
397	448	505	512	964	967	968	1108	1225	1225	1235	1324	1353	1361	1362	1363
49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5
45	45	45	45	45	45	45	45	45	45	45	45	45	45	45	2.
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 JUDGICI IN PRECURSOR - bovine NyAlternate names: antimicrobial peptide NyAlternate names: antimicrobial peptide Cispecies: Bos primigenius taurus (cattle) Cispecies: Bos primigenius taurus (cattle) Cispecies: Bos primigenius taurus (cattle) Cispecies: No. 16 torici, P.; Schode, Cispecies: No. 16 torici, P.; Schoder, Cispecies: No. 16 torici, No. 16 torici, No. 16 torici, No. 16 torici, Cattle Cispecies: No. 17 torici, No. 17 torici	Query Match 80.2%; Score 73; DB 1; Length 144; Best Local Similarity 100.0%; Pred. No. 0.0034; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 4 KWPWWPWRR 12 Db 135 KWPWWPWR 143	RESULT 2 VGING E2 glycoprotein precursor - human coronavirus (strain 229E) N;Alternate names: peplomer glycoprotein; S glycoprotein; spike glycoprotein C;Species: human coronavirus A;Note: host Homo sapiens (man) C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jun-2000 C;Accession: A34766; S05460 C;Accession: A34766; S05460 B;Raabe, T: Schelle-Prinz, B.; Siddell, S.G. J. Gen. Virol. 71, 1065-1073, 1990
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us-09-444-281-35.rpr

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Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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102 IKETPWWRWR 111
                                                                                                                                                                                                                                                                                                                                                            2 LKKWPWWPWR 11
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Best Local Similarity
Matches 5; Conserv
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A; Residues: 1-467 <STO>
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A, Map position: X
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A,Title: Nucleotide sequence of the gene encoding the spike glycoprotein of human corona A,Reference number: A34766; MUID:90264837; PMID:2345367
A,Accession: A34766; MUID:90264837; PMID:2345367
A,Accession: A34766; MUID:90264837; PMID:2345367
A,Roblecule type: MRNA
A,Residues: 1-1173 <-RAA>
A,Cross-references: EMBL:X16816; NID:958926; PIDN:CAA34723.1; PID:958927
A,Experimental source: strain 229E
R,Raabe, T: Siddell, S.
R,Raabe, T: Siddell, S.
Nucleic Acids Res. 17, 6387, 1989
A,Title: Nucleotide sequence of the human coronavirus HCV 229E mRNA 4 and mRNA 5 unique
A,Reference number: A34038; MUID:8936667; PMID:2701946
A,Accession: S05460
A,Accession: S05460
A,Residues: 1159-1173 <-RA2>
A,Cross-references: BmBL:X15654; NID:958921; PIDN:CAA33680.1; PID:gl334827
C,Reywords: glycoprotein; transmembrane protein
C,Reywords: glycoprotein; transmembrane #status predicted <-MAT>
F,1116-1138/Domain: signal sequence #status predicted <-MAT>
F,1116-1138/Domain: transmembrane #status pr
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C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999
B;Kawazabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jin-no, K.; Takah DNA Res. (33-101, 1999
A;Fitle: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Accession: B72492
A;Accession: B72492
A;Accession: B72492
A;Accession: B72492
A;Accession: B72492
A;Accession: B72492
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Cipate: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
Cipate: 23-Jul-1999 #sequence_revision 23-Jul-1999
Cipacession: T12505
Ribansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, June 1999
A;Reference number: 217527
A;Reference number: 217527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-299 <ANS>
A;Cross-references: EMBL;AL086753
A;Cross-references: adult testis; clone DKFZp434C192
C;Genetics: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein DKP2p434C192.1 - human (fragment)
C:Soecies: Homo sapiens (man)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.3%; Score 54; DB 1
85.7%; Pred. No. 9.1;
tive 0; Mismatches
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Pred. No. 6.1;
0; Mismatches
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ilarity 85.7%;
Conservative
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Best Local Similarity
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Matches 6; Conserv
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A, Accession: 17051
A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Experimental source: adrenal cortex
A, Experimental source: adrenal cortex
A, Mote: the authors translated the codon GTC for residue 205 as Gly
B, Sagara, Y., Takata, Y.; Miyata, T.; Hara, T.; Horluchi, T.
B, Sagara, Y., Takata, Y.; Miyata, T.; Hara, T.; Horluchi, T.
A, Title: Cloning and sequence analysis of adrenodoxin reductase cDNA from bovine adrena
A, Reference number: J70079
A, Title: Cloning and sequence analysis of PMID:3448086
A, Accession: J70079
A, Millian CONTAIN CONTAIN A, Millian CONTAIN CONTAINS A, Mote: the deduced sequence is partially confirmed by amino acid sequencing of 15 isol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein F18G5.2 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
C;Accession: E88605
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolc
A;Reference number: A75000; MUID:9966613; PMID:9851916
A;Note: see websites genome.wustl.ed/96sC/C_elegans/ and www sanger.ac.uk/Projects/C_el
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; ar
A;Cross-references: DDBJ:AP000064; NID:g5105945; PIDN:BAA81594.1; PID:d1045380; PID:g51 B;Experimental source: strain K1 C;Genetics: A;Genetics: A;Gene: APE2577
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Pred. No. 17;
0; Mismatches
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Pred. No. 11;
2; Mismatches
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probable moey protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B70741
R;Coloc, S.T; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamiln, N.; Holroyd, S.; Kajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Attle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MulD:98295987; PMID:9634230
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Nol. Biochem. Parasitol. 58, 161-164, 1993
A)Title: Cloning and sequence characterization of a complete myosin heavy chain cDNA fr
A;Reference number: A59287; MUID:93211444; PMID:8459827
A;Accession: A59287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:Z75555; GB:AL123456; NID:g3261608; PIDN:CAA99988.1; PID:e250356;
A;Experimental source: strain H37Rv
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C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 08-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown; translation not A;Molecule type: DNA
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                                               A;Accession: 833068
A;Molecule type: mRNA
A;Residues: 1-527 & SGO'>
A;Cross-references: EMBL:X65591
A;Nores-the authors translated the codon CAA for residue 346 as C;Superfamily: myosin heavy Chain; myosin motor domain homology C;Keywords: ATP; surface antigen
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F;82-752/Domain: myosin motor domain homology <MMO>
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             A;Reference number: A46514; MUID:93056536; PMID:1431131
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Pred. No. 69;
2; Mismatches
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Pred. No. 2
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Pred. No.
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Best Local Similarity 62.5%;
Matches 5; Conservative
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Matches 5; Conservative
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106 VLRNWPWW 113
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KRWAYYPWRR
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Matches 6; Conserv
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A.Reference mumber: J80390
A.Reference mumber: J80390
A.Rocesters = 180380
A.Rocesters = 180480
A.Rocesters = 180480
A.Rocesters = 180580
A.Rocesters = 180590
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A.Rocesters = 180580
A.Rocesters = 1805
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NiAlternate names: surface antigen, 200K
CiSpecies: Schistosoma mansoni
CiSpecies: Schistosoma mansoni
CiDate: 22-NOV-1993 #sequence_revision 06-Sep-1996 #text_change 13-Feb-1998
CiAccession, S33068
Risoisson, L.M.A.; Materson, C.P.; Tom, T.D.; McNally, M.T.; Lowell, G.H.; Strand, J. Immunol. 149, 3612-3620, 1992
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Matches 5; Conservative
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
F;8-190/Domain: short-chain alcohol dehydrogenase homology <SADH>
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A.Molecule type: DNA
A.Fesidues: 1.248 < PAR>
A.Cross references: EMBL:X60110
A.Accession: S24556
A.Molecule type: protein
A.Residues: 1.32 < PARI>
C.Genetics:
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A; Accession: T36208
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A; Gene: Rv0945
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A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, R.; Reference number: AB0502; MUD:21534947; PMID:11677608
A;Accession: AH0755
A;Stuts: preliminary
A;Molecule type: DNA
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C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T36208
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.submitted to the EMBL Data Library, May 1999
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A;Cross-references: GB:AL513382; PIDN:CAD05747.1; PID:916503239; GSPDB:GN00176
                                                                                                                                                                                                                          Apporthetical protein C50F7.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T2929
R;Johnson, D.; Stellyes, L.
Submitted to the RMEL Data Library, November 1995
R;Johnson, D.; Stellyes, L.
R;Accession: T29295
A;Reference number: Z20601
A;Reference number: Z20601
A;Reference number: L20601
A;Reference number: D20601
A;Reference number: DAAAAB3303.1; CESP:C50F7.8
A;References: EMBL:U41557; PIDN:AAAB3303.1; CESP:C50F7.8
A;Genetics:
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Best Local Similarity 75.0%; Pred. No. 6;
Matches 6; Conservative 0; Mismatches
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Best Local Similarity
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Cipecies: Mycobacterium tuberculosis
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A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Authors: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A7050; MUID:9829897; PMID:9634230
A; Accession: G70715
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A.Residues COLDA
A.Residues references: GB:279700, GB:AL123456; NID:G3261628; PIDN:CAB02005.1; PID:G1524217
A.Experimental source: strain H37Rv
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C;Species: Thermus aquaticus
C;Date: 22-dan-1993 #sequence_revision 22-Jan-1993 #text_change 30-Sep-2002
C;Accession: 823449; 824556
R;Park, H.J.; Kreutzer, R.; Reiser, C.O.A.; Sprinzl, M.
R;Park, H.J.; Kreutzer, R.; 1992
A;Title: Molecular coloning and nucleotide sequence of the gene encoding a H(2)O(2)-form A;Reference number: 823449; MUID:92249331; PMID:1577004
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Anlecule type: DNA
A;Residues: 1-114 <OLID
A;Cross-references: EMBL:AL049763; PIDN:CAB42078.1; GSPDB:GN00070; SCOEDB:SCE36.09
A;Experimental source: strain A3(2)
C;Genetics:
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C;Keywords: NAD; oxidoreductase
F;1-248/Product: NADH oxidase (H2O2-forming) #status experimental <MAT>
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Query Match 51.6%; Score 47; DB 2; Length 253; Best Local Similarity 100.0%; Pred. No. 18; Matches 5; Conservative 0; Mismatches 0; Indels
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RESULT 15

15.7754

histidinol-phosphate aminotransferase hisC-1 - Synechocystis sp. (strain PCC 6803)

NyAlternate names: protein sll1713

C; Species: Synechocystis sp.

C; Species: Synechocystis sp.

C; Avariety: PCC 6803

C; Accession: S77354

R; KaneKo, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

C; N.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

A; Reference number: S74322; MUID:97061201; PMID:8905231
A; Accession: S77354
A; Accession: S77354
A; Accession: S77354
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Ross-references: EMBL:D90906; GB:AB001339; NID:g1652492; PIDN:BAA17457.1; PID:g165253
A; Cross-references: EMBL:D90906; GB:AB001339; NID:g1652492; PIDN:BAA17457.1; PID:g165253
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Genetics:
A; Genetics:
C; Superfamily: probable histidinol-phosphate transaminase

5; Gaps Query Match

51.1%; Score 46.5; DB 2; Length 352;
Best Local Similarity 50.0%; Pred. No. 29;
Matches 8; Conservative 1; Mismatches 2; Indels 5

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Search completed: May 4, 2004, 15:22:58 Job time: 12.9737 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bonavia A. . Holmes K.V.; with which cell line persistently infected "Viral and cellular changes in a human cell line persistently infected with human coronavirus HCOV-229E."; submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=90264837; PubMed=2345367;
Raabe T., Schelle-Prinz B., Siddell S.G.;
Nucleotide sequence of the gene encoding the spike glycoprotein of human coronavirus HCV 229E.";
J. Gen. Virol, 71:1065-1073(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21262210; PubMed=11369870;
Thiel V., Herold J., Schelle B., Siddell S.G.;
"Infectious RNA transcribed in vitro from a cDNA copy of the human
coronavirus genome cloned in vaccinia virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human coronavirus (etrain 229E) (HCOV-229E).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
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16479 MW; E3B1CBBE55C09911 CRC64;
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MEDLINE=22440020; PubMed=12551991;
Bonavia A., Zelus B.D., Wentworth D.E., Talbot P.J., Holmes K.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
E2 glycoprotein precursor (Spike glycoprotein) (Peplomer protein)
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STRAIN=Isolate RW Stock, Isolate P100E, Isolate P11A, and
Isolate P11B;
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STRAIN=ISOSIATE ATCC VR-74, ISOSIATE A162, and ISOSIATE LRI
MEDIINE-SOS(140;) PubMed=9870593;
Hays J.P., Myint S.H.;
Hays J.P., Myint S.H.;
"PCR sequencing of the spike genes of geographically and chronologiantly distinct human coronaviruses 229E.";
J. Virol. Methods 75:179-193(1998).
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Nucleic Acids Res. 17:6387-6387(1989)
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J. Gen. Virol. 82:1273-1281(2001).
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Gallagher T.M., Buchmeier M.J.;

Virology 279:371-374(2001).

-I- FUNCTION: Structural protein that makes spikes at the surface of the virus. Initiates infection by specifically recognizing and binding the human aminopeptidate ANPEP receptor. Its association with ANPEP may lead to its conformational change that triggers fusion between viral and host cellular membrane.

-I- SUBUNIT: Homotrimer, During virus morphogenesis, it is found in a complex with M and HE proteins (By similarity). Interacts with
Udentification of a receptor-binding domain of the spike glycoprotein of human coronavirus HCoV-229E."; J. Virol. 77:2530-2538(2003).
                                                                                                                                     MEDLINE=22521439; PubMed=12634402; Breslin J.J., Mork I., Smith M.K., Vogel L.K., Hemmila E.M., Bonavia A., Talbot P.J., Sjoestrom H., Noren O., Holmes K.V.; "Human coronavirus 229E: receptor binding domain and neutralization by soluble receptor at 37 degrees C."; J. Virol. 77:4435-4438(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- DOMAIN: The spike S1 domain displays the specificity for the host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Y09923; CAA71056.1; -.
EMBL; Y09923; CAA71056.1; -.
EMBL; X10651; CAA71146.1; -.
EMBL; X10651; CAA71146.1; -.
EMBL; X15654; CAA33680.1; -.
InterPro; IRR002551; Corona_S1.
InterPro; IRR002552; Corona_S2.
Ffam; PP01600; Corona_S1; 1.
Ffam; PP01601; Corona_S1; 1.
Virulence; Glycoprotein; Envelope protein; Transmembrane; Signal; Coiled coil.
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EXTRACELLULAR (POTENTIAL)
POTENTIAL.
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EMBL, AF3044186; AAK32188.1; --
EMBL, AF344187; AAK32189.1; --
EMBL, AF344189; AAK32190.1; --
EMBL, AF344189; AAK32191.1; --
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us-09-444-281-35.rsp

PT VARIANT 775 775 A -> S (in isolate A162).  Query Match Best Local Similarity 85.7%; Pred. No. 4.2;  Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  Qy 4 KWHWWWW 10  Db 1113 KWPWWVW 1119			RN 13)  RN MEDLINE=87200696; PubMed=3038094;  RA MEDLINE=87200696; PubMed=3038094;  RA Nonaka Y., Murakami H., Yabusaki Y., Kuramitsu S., Kagamiyama H.,  RA Nonaka Y., Okamoto M.;  RA Monaka Y., Okamoto M.;  RA Manno T., Okamoto M.;  RI Molecular cloning and sequence analysis of full-length cDNA for mRNA RT datenodoxin oxidoreductase from bovine adrenal cortex.";  RI Biochem. Biophys. Res. Commun. 145:1239-1247(1987).  RA HOLINE=8710752; PubMed=2924777;  RA MEDLINE=8710752; PubMed=2924777;  RA MANNEOGIU I., Guttinger T.;  RA Hanukoglu I., Guttinger T.;  RT "CDNA sequence of adrenodoxin reductase. Identification of NADP-RI Education 180:479-484 (1989).	
(GLCNAC ) (		N-LINKED (GLCNAC) (POTENTIAL). N-LINKED (GLCNAC) (POTENTIAL). N-LINKED (GLCNAC) (POTENTIAL). N-LINKED (GLCNAC) (POTENTIAL). N -> S (in isolate LRI 281). N -> I (in isolate LRI 281). LR -> IS (in isolate A162). N -> T (in isolate A162). T -> N (in isolate A162). T -> N (in isolate A162). C -> V (in isolate LRI 281). C -> P (in isolate LRI 281). C -> P (in isolate LRI 281).	Floub and AlCC Ve /4).  S -> X (in isolate Al62).  D -> X (in isolate P100B).  V -> A (in isolate B100B).  T -> M (in isolate B100B).  T -> M (in isolate Al62).  PQ -> LR (in isolate Al62).  PQ -> LR (in isolate Al62).  ROSENCYPAG -> VGRCYNCRPAV (in isolate Al62).  K -> M (in isolate LR 2B1).  KYVAVYANYG -> QFVGAKED (in isolate Al62).  K -> M (in isolate Al62).  WAYSKYYT -> LANLNSHN (in isolate Al62).  S -> T (in isolate Al62).  G -> V (in isolate Al62).  C -> V (in isolate Al62).	V -> A (in isolate LRI 281). V -> N (in isolate A162). V -> N (in isolate A162). L -> V (in isolate A162). L -> V (in isolate A162). L -> M (in isolate A162). L -> T (in isolate P11A). V -> G (in isolate P11A). V -> G (in isolate P11B). T -> M (in isolate A162). T -> M (in isolate A162). T -> M (in isolate A162). L -> I (in isolate A162). L -> I (in isolate A162). C -> N (in isolate A162).
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1136 23 622 98 1147 1171 1256 226	100200 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 100000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 100000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 100000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 100000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 100000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000	1066 10082 10082 10082 1208 127 127 2210 223 230	22228888888888888888888888888888888888	44444 44444 44444 5530 5530 66812 700 711 711 72 74 75 75 75 75 75 75 75 75 75 75 75 75 75
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Pred. No. 8.7;
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                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF COWPLEX WITH ADRENODOXIN.
MEDLINE=2164735; PubMed=11053423;
MEDLINE=21164735; PubMed=11053423;
Meller J.J., Lapko A., Bourenkov G., Ruckpaul K., Heinemann U.;
"Adrenodoxin reductase-adrenodoxin complex structure suggests electron transfer path in steroid blosynthesis.";
J. Biol. Chem. 276:2786:2789(2001).
I. Biol. Chem. 276:2786:2789(2001).
Intochondrial p450 systems. Including cholesterol side chain cleavage in all steroidogenic tissues, steroid 11-beta hydroxylation in the Aidney, and sterol C-27 hydroxylation in the
      X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
MEDLINE=22455764; PubMed=10998235;
Ziegler G.A., Schulz G.E.;
"Crystal structures of adrendoxin reductase in complex with NADP+ and NADPH suggesting a mechanism for the electron transfer of an enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NADPH ADRENDOXIN OXIDOREDUCTASE.

E -> EVLLLCQ (in isoform Long).

Fyrid=Vey 003415.

G -> R (IM REF. 3).

FGVAPDHPEVKNVI -> VWLALTTPRSRMLL (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             msoid=P08165-2; Sequence=VSP 003415;
Note=Represents 10-20% of all adrenodoxin reductase mRNAs and
seems to be inactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAAGIRLAVTR -> ARRSAWQSPE (IN REF. 3)
                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: Reduced adrenodoxin + NADP(+) = oxidized
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ditochondrion; FAD; Flavoprotein; NADP; Transit peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                       adrenodoxin + NADPH.
-!- COFACTOR: FAD.
-!- PATHWAY: Cholesterol side-chain-cleavage system.
-!- SUBUNIT: Monomar.
-!- SUBCELULLAR LOCATION: Mitochondrial matrix.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
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IsoId=P08165-1; Sequence=Displayed;
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32 MITOCH
CHAIN 33 492 NADEH:
VARSPLIC 204 204 E-> E
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                                                                                                                                                                                                                                                                                                                                                                                                      ABLINE=9825987; PubNed=9634230; Garnier T., Churcher C., Harris D., Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eglameier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Comnor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Horney T., Jagels K., Krogh A., McLen J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Squares R., Bolipering the biology of Mycobacterium tuberculosis from the complete genome sequence."
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MEDLINE=2220644; PubMed=12218036;

Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O.,

Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,

Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,

Bishal W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;

"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laboratory strains.";
J. Bacteriol. 184:5479-5490(2002).
-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
                                                                                                                                                                                                           Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Putative oxidoreductase Rv0945/MT0971 (EC 1.-.-).
RV0945 OR MT0971 OR MTCX10D7.29C.
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EMBL; AE006982; AAK45219.1; -.
PIR; G70715; G70715.
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas., Barry C.E. III, Frekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Geger K., Skelton S., Squares S., Squares R., Selfon J.E., Skelton S., Squares R., Stelton S., Squares R., Selfon S., Squares C., Roberte Genome sequence.";

Nother S., Seguence.";
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MEDLINE=2220644; PubMed=1218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., Hickey E.,
Eterson J., DeBoy R., Dodson R., Gwinn M., Hatt D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishal W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
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                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium,
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InterPro; IPR00554; ThiF_domain.
Pfon, PF00899; ThiF; Complete proteome.
SEQUENCE 715 AA; 78181 MW; 455495248A56041C CRC64;
                                                                                                                                                                                    01-0CT-1996 (Rel. 34, Created)
01-0CT-2096 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
NUJSEC OR MIJ398 OR MICYOZBIO.19C.
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PIR; B70741; B70741.
TIGR; MT1398; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laboratory strains.";
J. Bacteriol. 184:5479-5490(2002)
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TIGN; MT0971; -.
Tuberculist; Rv0945; -.
Tuberculist; Rv0945; -.
Tuberculist; Rv0945; -.
Pinterpro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
PROSTTE; PS00061; ADH_SHORT; 1.
PROSTTE TRANSPORT TO THE T
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                                                                                                                    SEQUENCE FROM N.A.

MEDIINE=89386000; PubMed=2550899;

MEDIINE=89386000; PubMed=2550899;

Jordi B.U.A.M., Kremers D.A.W.M., Kusters H.G., van der Zeijst B.A.M.,

"Nucleotide sequence of the gene coding for the peplomer protein (=
spike protein) of infectious bronchitis virus, strain D274.";

Nucleot Acids Res. 17.6726-6726 (1389).

-I. FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF VIRIONS
TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION.
                                                                        Avian infectious bronchitis virus (strain D274) (IBV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                        (Peplomer protein)
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P12722; Q66176; Q66177;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
E2 glycoprotein precursor (Spike glycoprotein) (if Contains: Spike protein S1; Spike protein S2].
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RESULT 6
VGL2 IBVD2
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MEDLINE=85159540; PubMed=2984314;
Binns M.M., Boursnell M.E.G., Cavanagh D., Pappind D.J.C.,
Brown T.D.K.;
"Cloning and sequencing of the gene encoding the spike protein of the coronavirus IBV.";
                                                                                                                    Gaps
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-I. PUNCTION: THE PERLOWER PROTEIN MEDIATES THE BINDING OF VIRIONS TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Avian infectious bronchitis virus (strain Beaudette) (IBV). Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                               RESULT 7
VGL2 IBVB

VGL2 IBVB

TD VGL2 IBVB

AC P11223; P06134;

DT 01-UUL-1989 (Rel. 11, Created)

DT 01-UUL-1989 (Rel. 11, Last sequence update)

DT 15-MAR-2004 (Rel. 143, Last annotation update)

DE E2 glycoprotein precursor (Spike glycoprotein) (Peplomer protein)

DE (Contains: Spike protein S1; Spike protein S2].
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1154 AA; 127502 MW; D79F37AF89F1A37F CRC64;
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                                                                Score 46.5; DB 1; Length 1154; Pred. No. 42; 1; Mismatches 1; Indels 3.
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DR EMBL; M95169; CAA26201.1; -.
DR PIR; S14939; CAA26201.1; -.
DR PIR; S14939; CAA26201.1; -.
DR PIR; S14939; CACODA S1.
DR FIGHT, PR002552; Corona S2.
DR PFGM; PF01600; Corona S1; 1.
The Sfam; PF01600; Corona S2; 1.
The Sfam; DR02500; Corona S2; 1.
The Sfam; DR02500; Corona S2; 1.
The Sfam; DR02500; Corona S2; 1.
The CHAIN 19 1162 ED CLEONOTEIN S1.
THE CHAIN S38 1162 SPIKE PROTEIN S2.
THE DOMAIN 1120 1137 CYS-RICH.
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Best Local Similarity 61.5%;
Matches 8; Conservative
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FT CARBOHYD 247 247 N-LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 264 264 N-LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 266 306 N-LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 306 306 N-LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 513 513 N-LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 530 530 N-LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 530 530 N-LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 591 591 N-LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 592 579 N-LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 593 N-LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 594 N-LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 596 N-LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 1014 N-LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 1034 N-LINKED (GLCNAC	1 ILKKWPWWPW 10	VGL2_IBVK  TD VGL2_IBVK  AC P12650;  DT 01-0CT-1989 (Rel. 12, Created)  DT 01-0CT-2001 (Rel. 40, Last sequence update)  DT 16-0CT-2001 (Rel. 40, Last annotation update)  DE B2 glycoprotein precursor (Spike glycoprotein)  DE (Contains: Spike protein S1; Spike protein S2].	Servian infectious bronchitis virus (strain KB8523) (IBV).  OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; OC Coronaviridae; Coronavirus. OX NCBI_TaxID=11126; RN [1] RP SEQUENCE FROM N.A. RX MEDLINE=88306251; PubMed=2841803; RA Struct. S., Sato S., Okabe T., Nakai M., Sasaki N.; RT "Cloning and sequencing of genes encoding structural proteins of RT avian infectious bronchitis virus.";	Preparing Structure of the Carter of the Car	CC

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Binns M.M., Boursnell M.B.G., Tomley F.M., Brown T.D.K.; "Comparison of the spike precursor sequences of coronavirus IBV strains M41 and 6/82 with that of IBV Beaudette."; J. Gen. Virol. 67.282-2831(1986).
-i. FUNCTION: THE PRELOMER PROTEIN MEDIATES THE BINDING OF VIRIONS TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 1163;
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SPIKE PROTEIN S1
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61.5%; Pred. No. 42;
iive 1; Mismatches
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InterPro; IPR002551; Corona_S1.
InterPro; IPR002551; Corona_S2.
Pfam; PF01601; Corona_S2; 1:
Pfam; PF01601; Corona_S2; 1:
Glycoprotein; Transmembrane; Signal.
SIGNAL 1 18 E2 GLYCOP;
CHAIN 19 1163
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Coronaviridae; Coronavirus.
[1] TaxID=11121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.AUG-1987 (Rel. 05, Created)
13.AUG-1987 (Rel. 05, Last sequence update)
15.ARA-2004 (Rel. 43, Last and tation update)
E2 glycoprotein precursor (Spike glycoprotein) (Peplomer protein)
[Contains: Spike protein S1, Spike protein S2].
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Pred. No. 42;
1; Mismatches 1; Indels 3;
                                                EMBL, M21883; AAA66575.1; -.
EMBL, A24863; CAA01736.1; -.
PIR: S07421; S07421
InterPro; 1PR002551; Corona_S1.
Pfam: PF01600; Corona_S1: 1.
Pfam: PF01601; Corona_S1: 1.
Pfam: PF01601; Corona_S2: 1.
Square PF01601; Corona_S2: 1.
Pfam: PF01601; Corona_S2: 1.
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SPIESE PROTEIN S1.
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SEQUENCE FROM N.A.
MEDLINE=87085499; PubMed=3025348;
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DT 10-0CT-2003
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GN MYCObacteriu
OS MYCObacteriu
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Pred. No. 9.3;
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196 AA; 22104 MW; 436764DA9E26074C CRC64;
                                                                                                                            Eukaryota, Fungi, Ascomycota, Schizósaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
01-NCV-1995 (Rel. 32, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Propchetical protein C5H10.05c in chromosome I.
SPACSH10.05C
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15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
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                                                                                                    Schizosaccharomyces pombe (Fission yeast)
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InterPro; IPR003680; NADHdh 2.
Pfam; PF02525; Flavodoxin_2; 1.
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Best Local Similarity 47.12

Then 8; Conservative
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                                                                                                                                                                                  Schizosaccharomyces
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SEQUENCE FROM N.A.

STRAIN=21927647; Pubmed=11930014;

SIEGRATE A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,

Slegarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,

A Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,

A Shcherbinina O.V., Kozavkin S.A.,

Malykh A.G., Koonin E.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,

A Malykh A.G., Koonin E.V., Kozavkin S.A.,

The complete genome of hyperthermophile Methanopyrus kandleri AV19

and monophyly of archaeal methanogens.", 99:4644-4649(2002).

Proc. NaII. Acad. Sci. U.S.A. 99:4644-4649(2002).

-I- FUNCTION: Modulates the activity of chromatin proteins, thereby

C -I- CHALNTIC ACTIVITY: NAD(+) + an acetylprotein = nicotinamide + O-

acetyl-App-ribose + a protein.

-I- COFACTOR: Binds 1 zinc ion and NAD (By similarity).

-I- SUBCELLULAR LOCATION: Cytoplasmic (Probable).

-I- SIMILARITY: Belongs to the sirtuin family.
                                                                                                                                            NPDA OR MK1075.
Methanopyrus kandleri.
Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
15-MAR-2004 (Rel. 43, Last annotation update)
NAD-dependent deacetylase (EC 3.5.1.-) (Regulatory protein SIR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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Transcription regulation; Hydrolase; NAD; Metal-binding; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 40, Last annotation update)
10-0CT-2003 (Rel. 40, Rel. 40, 
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BY SIMILARITY.
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 46; DB 1
Pred. No. 12;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 397 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE010396; AAM02288.1; -.
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InterPro; IPR003000; SIR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 54.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134
125
151
151
154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 1
250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete protecme
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gavastanoi.";
J. Bacteriol. 173:463-471(1991).
-!-CATALYTIC ACTIVITY: Chorismate + L-glutamine = anthranilate +
pyruvate + L-glutamate.
-!- PATHWAY: Tryptophan biosynthesis; first step.
-!- PATHWAY: Tryptophan biosynthesis; first step.
-!- SUBUNIT: Tetramer of two components I and two components II (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Cederberg H., Hohmann S., Schaaff-Gerstenschlaeger I., Huse K.,
Zimmermann F.K.;
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                            SECUENCE FROM N.A. MEDILINE=9110031, PubMed=1987141, MEDILINE=91100331, PubMed=1987141, MEDILINE=91100331, PubMed=1987161, Molecular Silva O., Kosuge T.; Molecular characterization and expression analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , DB 1, Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                    anthranilate synthase gene of Pseudomonas syringae subsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56084 MW; A38E81931331F6BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Probable transporter FENZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      512 AA
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Best Local Similarity 71.4%; Pred. No. 31;
Matches 5; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interror, IPRO05258; .... IN; 1.
Fiam; PR04715; Anth synt IN; 1.
Pfam; PR00425; Anth synt In; 1.
PRINTS; PR00095; ANTSNITASEI.
PRODOM; PD000779; Anth synth chor; 1.
ProDom; PT0R00564; trpE most; 1.
"TOPRAMS; TIGR00564; trpE most; 1.
"TOPRAMS; TIGR00564; trpE most; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR005801; Anth synth chor. InterPro; IPR006805; Anth-synth I.N. InterPro; IPR005265; Anth-synth I.N. InterPro; IPR005265; Anth-synth I.N. InterPro; IPR005265; Anth-synth I.N. InterPro; IPR005265; Anth-synth I.N. INTERPROSE INTERPRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=93070619; PubMed=1332309;
                              Pseudomonadaceae; Pseudomonas NCBI_TaxID=29438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M55911; AAA26016.1; -.
HSSP; Q06128; 1QDL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  485 WWPWPRR 491
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FEN2_YEAST
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MEDLINE=22206494, PubMed=12218036,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Eaft D., Hickey E.,
Feterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Blishai W., Jacobe W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                          MEDLINE=9829587; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd (Horsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Gall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laboratory strains.";

0. Bacteriol. 184:5479-5490(2002).

-!- SUBCELLUAR LOCATION: Integral membrane protein (Potential).

-!- SIMILARITY: Belongs to the mmpL family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; Complete proteome.
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01-MAY-1991 (Rel. 18, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anthranilate synthase component I (EC 4.1.3.27).
TRPE.
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EMBL; AE007027; AAK45875.1; --
PIR; B70763; B70763.
TIGR; MI1608; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tuberculist, Rv1557; -.
InterPro; IPR004869; MMPL.
Pfam; PF03176; MMPL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                        SEQUENCE FROM N.A.
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P21689;
01-MAY-1991 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF03176
Hypothetical
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TRPE PSESS
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DT 01-MAY
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                                                                                                                                                                                                                                                                                                                                       resistance.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: Belongs to the allantoate permease family.
               Lucchini G.;
"Nuclocide sequence of 9.2 kb left of CRY1 on yeast chromosome III
"Inclocide sequence of 9.2 kb left of a final section and functional
analysis of open reading frame YCR28.";
Yeast 8:805-812(1992).
Carbone M.L.A., Panzeri L., Falconi M.M., Carcano C., Plevani P.,
                                                                                                                                                                                                                        MEDLIKE=96367594; PubMed=8771708; Marcireau C., Joets J., Pousset D., Guilloton M., Karst F.; "FENZ: a gene implicated in the catabolite repression-mediated regulation of ergosterol biosynthesis in yeast."; Yeast 12:531-539(1996).
-!- FUNCTION: Involved in the catabolite repression-mediated regulation of ergosterol biosynthesis and in fenpropimorph
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GO; GO:0015233; F:pantothenate transporter activity; IGI.
GO; GO:0015887; P:pantothenate transport; IGI.
Transmembrane; Transport.
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W - v (IN REF. 2).
                                                                                                           SIMILARITY TO DALS FAMILY.
MEDLINE=94147996; PubMed=8313894;
Koonin E.V., Bork P., Sander C.;
"Yeast chromosome III: new gene functions.";
EMBO J. 13:493-503(1994).
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512 AA;
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2; Mismatches

Search completed: May 4, 2004, 15:20:16 Job time : 9.21053 secs

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Okamoto H., Nishizawa T., Tawara A., Peng Y., Takahashi M.,
Kishimoto J., Tanaka T., Miyakawa Y., Mayumi M.;
Kishimoto J., Tanaka T., Miyakawa Y., Mayumi M.;
Specise-specific TT viruses in humans and nonhuman primates and their
phylogenetic relatedness.";
Virology 277:368-378(2000)
EMBL; AB041959; BAB19313.1;
EMBL; AB041959; BAB19313.1;
GO; GO:0004185; F:serine carboxypeptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001563; Peptidase_S10.
InterPro; IPR00419; Trvirus_Unk.
Pfam; PF02956; TT ORFI; I:
PROSITE; PS00131; CARBOXYBET SER SER; I.
SEQUENCE 723 AA; 85393 MW; 23ZD003098766344 CRC64;
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Viruses, ssDNA viruses, Circoviridae, Anellovirus.
NCBI_TaxID=68887;
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Q7U074
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00947V5
009D186
02D180
08DVT9
08ZN02
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SEQUENCE FROM N.A.
STRAIN=ME-TIV9;
MEDLINE=2053933; PubMed=11080484;
  Q9DUC4;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2003 (TrEMBLrel. 25,
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transmissible gastroenteritis virus."; J. Gen. Virol. 74:1795-1864(1993).
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01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
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nes 6; Conservative
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                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group).
Wakaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales; Poaceae;
Enrhartoideae, Oryzeae,
                                                                                                                                                                                                                                                                                                                         Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overton II L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S., Radmuller S.B., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., Mitte O., Salzberg S.L., Fraser C.M., G.M., Salzberg S.L., Fraser C.M., Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duarte M., Laude H.; "Sequence of the porcine epidemic diarrhoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93389433; PubMed=8397280;
Bridgen A., Duarte M., Tobler K., Laude H., Ackermann M.;
"Sequence determination of the nucleocapsid protein gene of the porcine epidemic diarrhoea virus confirms that this virus is a coronavirus related to human coronavirus 229E and porcine
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EMBL; AAC120535; AAC13229.1; -.
Hypothetical protein.-15795 WW; 67E62CFAD153CB99 CRC64;
SEQUENCE 137 AA; 15795 WW; 67E62CFAD153CB99 CRC64;
                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein OSJNBa0092N01.27.
OSJNBA0092N01.27.
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SEQUENCE FROM N.A.
MEDLINE=94231173; PubMed=8176382;
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Buell R.;
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"Sequence analysis of the porcine epidemic diarrhea virus genome between the nucleocapsid and spike protein genes reveals a polymorphic
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MEDLINE-98455678; PubMed=9782358;
Bridgen A., Kochernann R., Tobler K., Carvajal A., Ackermann M.;
Britcher analysis of the genome of porcine epidemic diarrhea virus.";
Adv. Exp. Med. Biol. 440:781-786(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                            "Sequence analysis of the porcine epidemic diarrhea virus genome between the nucleocapsid and spike protein genes reveals a polymo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; SsRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
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J. Gen. Virol. 74:1795-1804(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
SEQUENCE FROM N.A.
MEDLINE=94120721; PubMed=8291230;
Duarte M., Tobler K., Bridgen A., Rasschaert D., Ackermann M.,
Laude H.;
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Duarte M., Tobler K., Bridgen A., Rasschaert D., Ackermann M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 54; DB 12; Length 1383;
Pred. No. 42;
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Kocherhans R., Bridgen A., Ackermann M., Tobler K.;
"The complete genome sequence of porcine epidemic diarrhea
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741C84D5DD3BDC4D CRC64;
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Last annotation update)
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MEDLINE=96112302; PubMed=8830538;
Tobler K., Ackermann M.;
TEDY leader sequence and junction sites.";
Adv. Exp. Med. Biol. 380:541-542(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                   Detween the micleocapsid and spike Virology 198:466-476(1994).

EMBL, 225483; CAA80971.1; -.

INTELPT: IPR002551; Corona_S1.

InterPr: IPR002552; Corona_S2.

Pfam; PF01601; Corona_S2; 1.

Pfam; PF01601; Corona_S2; 1.

Pfam; PF01601; Corona_S2; 1.

Promit T 42.

SEQUENCE 1383 AA; 151405 MW; 7,
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MEDLINE=93389433; PubMed=8397280;
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InterPro; IPR002552; Corona_82.
Pfam; PF01600; Corona_81; 1.
Pfam; PF01601; Corona_82; 1.
SEQUENCE 1386 AA; 151853 MW; 11F99BCB2AA0526B CRC64;
                                                                                                                                                                                                                                                                                 Created)
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EMBL; AE012475; AAM42819.1; -.
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01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
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                                                                                                                                                                                                                                                                                                                               nner membrane protein.
                                                                                                                                                                    1325 KWPWWW 1331
                                                         Query Match
Best Local Similarity
Local 6; Conserve
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Q8P4Z9;
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1D QBPPUS
AC QBPPUS
DT 01-0C
DT 01-0C
DT 01-0C
DT XACOS
CS XAURI
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Kang T.-J., Lim Y.-Y., Jang Y.-S., Kwon T.-H., Kim D.-H., Yang M.-S., "Spike Protein gene of Korea Porcine Epidemic Diarrhea Virus.";
Submitted (ARR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AF500215; AAM19716.1; -.

InterPro, IPR002551; Corona_S1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Chinju99;
STRAIN=Chinju99;
Cloning and nucleotide sequence analysis of spike gene of porcine epidemic diarrhea virus detected in Korea.";
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ANIG585; ANNOS521.1;
InterPro; IPR002551; Corona_S1.
Pfam; PF01600; Corona_S1.
Pfam; PF01600; Corona_S1; 1.
BEAN; PF01601; Corona_S1; 1.
SEQUENCE 1383 AA; I51582 MW; B5BA4D7EB5371A54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
NCBI_TaxID=28295;
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Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
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                                                                                                                                     Score 54; DB 12; Length 1383; Pred. No. 42; 0; Mismatches 1; Indels (
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Pred. No. 42;
                          EMBL; AR3353511; AAK38656.1; -...
InterPro; IPR002551; Corona_S1.
InterPro; IPR002552; Corona_S2.
Pfam; PF01600; Corona_S1; 1.
Pfam; PF01601; Corona_S2; 1.
SEQUENCE 1383 AA; I51352 MW; 022E5E5E5435876D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
             Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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Q8QQ98,
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequ
01-OCT-2002 (TrEMBLrel. 22, Last sequ
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Porcine epidemic diarrhea virus
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85.7%;
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Best Local Similarity 85.70,
Best Local Similarity 65.70
                                                                                                                                   Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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SEQUENCE FROM N.A.

STATIS—ATCC 33913 / NCPPB 528;

MEDLINE=22022145; PubMed=12024217;

MEDLINE=22022145; PubMed=12024217;

A a Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A lves L.M.C., do Amaral A.M., Bertolnin M.C., Camargo L.B.A.,

A lves L.M.C., do Amaral A.M., Bertolnin M.C., Camargo L.B.A.,

Camarotte G. Cannavan F., Cardozo J., Chambergo F.C., Ciapina L.P.,

Cararelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

Paria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rosei N.M.,

Martins E.C., Machados M.A., Madeira A.M.B.N., Martinez-Rosei N.M.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Spinoda L.A.F., Tarkita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

Spinoda L.A.F., Tarkita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

Setubal J.C., Kitajima J.P.,

Comparison Of the genomes of two Xanthomonas pathogens with differing
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Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
Xanthomonadacee; Xanthomonas.
NCBI TaxID=340;
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Bacteria, Yanthomonadales;
59.3%; Score 54; DB 12; Length 1386; larity 85.7%; Pred. No. 42; Conservative 0; Mismatches 1; Indels
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Local Similarity 71.4%; Pred. No. 7.3;
les 5; Conservative 1; Mismatches 1; Indels
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Last annotation update)
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01-0CT-2002 (TrEMBLrel, 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Inner membrane protein.
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Xanthomonadaceae; Xanthomonas.

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Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDILINE-20456801; PubMed-11003468;
Ukita M., Okamoto H., Nishizawa T., Tawara A., Takahashi M.,
Iizuka H., Miyakawa Y., Mayumi M.;
"The entire nucleotide sequences of two distinct TI virus (TTV)
isolates (TJN01 and TJN02) remotely related to the original TTV
isolates.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.1%; Score 52; DB 12; Length 746; 66.7%; Pred. No. 43; 2; Indels Aative 1; Mismatches 2; Indels
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Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
NCBI_TaxID=2303;
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arch. Virol. 145:1543-1559(2000).
EMBL, AB028669; BAA94878.1; -.
Interpro; IPRO04219; Tuvirus Unk.
Pfan; PRO2956; TT_ORF1; 1.
SEQUENCE 746 AA, 88561 MW; E0B22953AE764E3E CRC64;
                                                                                                                                                     Last sequence update)
Last annotation update)
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                      Viruses, ssDNA viruses; Circoviridae; Anellovirus.
VCBI_TaxID=68887;
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                                                           746 AA
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                                                                                                                           Created)
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MEDLINE=20479972; PubMed=11029001;
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EMBL, AL445064; ACGI1612.1; -
Interpro; IPR000731; SSD, STM.
PROSITE; PS50156; SSD; 1.
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Matches 6; Conservative
                                                           PRELIMINARY;
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SEQUENCE 1018 AA
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                                                                                                                                                                                                                                            TT virus.
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                                                        09JH31
09JH31;
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RESULT 10
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                STRAIN=306 / ATCC 13902 / XV 101;

STRAIN=306 / ATCC 13902 / XV 101;

MEDLINE=22022145; PubMed=12024217;

A a Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A aves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.S.A.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.S.A.,

A alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.S.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciaphna L.D.,

Caraclli R.M.B., Coutinho L.L., Cureino-Santos J.R., Elborry H.,

Paria J.B., Ferraco M.C., Greggio C.C., Ferro M.I.T.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

Locali E.C., Machado M.A., Madeira A.M.B.M., Martinez-Rossi N.M.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.B., Teixeira B.C., Tezza R.I.D.,

A prindade dos Santos M., Truffi D., Teai S.M., White F.F.,

Setubal J.C., Kitajima J.P.;

St. "Comparison of the genomes of two Xanthomonas pathogens with differing

Not specificaties.",
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MEDLINE=22225144; PubMed=12240834;
MRDLINE=22225144; PubMed=12240834;
Makamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto (Matanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
DNA Res. 9:123-130(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QBDJH5, PRELIMINARY; PRT; 351 AA. QBDJH5; 01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-JNA-2003 (TrEMBLrel. 24, Last annotation update) Tirl250 protein.
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InterPro; IPR001678; Sun Nop1/Nop2.
Pfam, PF01189; No11_Nop2_Sun; 1.
Complete protecme.
SEQUENCE 351 AA; 38494 MW; 67506
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EMBL; AE011686; AAM35479.1; -.
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SEQUENCE 105 AA;
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SEQUENCE FROM N.A.
Spiegel L.A., King L., Kirchoff K.A., de la Bastide M., Preston R.R., Napiegel L.A., King L., Kirchoff K.A., Miller B., Cunnius D.M., Nacionacione. Lu. Vil M.D., Baker J.P., Miller B., Cunnius D.M., Shatk K.H., Rodriquez S., Santos L., Zutavern T., Balija V.S., Shah R.S., Bahret A., Bal H.P., O'Shaughnessy A., Dedhia N.N., McCombie W.R.;
"Genomic Sequence For Oryza sativa, Nipponbare Strain, Chromosome X, "Genomic Sequence For Oryza sativa, Nipponbare Strain, Chromosome X, Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ACO82945, AAK13143.1;
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Enrhartoldeae, Oryzeae, Oryza.
                                                                                                                                                                                                                                             084ZR3;
01-UTW-2003 (TERMELrel. 24, Created)
01-UTW-2003 (TERMELrel. 24, Last sequence update)
01-UTW-2003 (TERMELrel. 24, Last annotation update)
01-UTW-2003 (TERMELrel. 24, Last annotation update)
01-UTW-2012 (TERMELrel. 24, Last annotation update)
01-17 (Japonica cultivar-group)
07-Yza Sativa (Japonica cultivar-group)
07-Yza Sativa (Japonica cultivar-group)
07-Yza Spermatophyta; Uridiplantae; Streptophyta; Embryophyta; Poaceae;
Ehrhartoldeae; Oryzae; Oryza.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE TO Nipponbare;
SEGAIN=cv. Nipponbare;
SEGAIN=cv. Nipponbare;
SEGAIN=cv. Natsunctor T., Yamamoto K.;
SOLYZA SALIVA nipponbare(GA3) genomic DNA, chromosome 7, BAC clone.COLID-2010],
Submitted (JTL-2010) to the EMBL/GenBank/DDBJ databases.
EMBL, APO03227; BACS7651.1; -
SEGAIL, APO03227; BACS7651.1; -
SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL SEGAIL 
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Hypothetical protein.
SEQUENCE 327 AA; 36672 MW; SCCA9080664BDOCA CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
0SJNBA0058E19.18.
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6; Conservative
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Q84ZR3
Matches
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Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).

EMBL, AE009902; AAL64549.1; -.

GO, GO:0009156; F:dihydropteroate synthase activity; IEA.

GO, GO:0009396; P:follc acid and derivative biosynthesis; IEA.

InterPro: IPR000489; Dhfropt_synth.
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STRAIN=IM2 / ATCC 51769 / DSM 7523;
MEDLINE=21664397; PubMed=11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ansorge W., Wirkner U., Mewes H.W., Gassenhuber J., Wiemann S., Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; 712505; 712505; 712505. PIR.; 712505; Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ilarity 71.4%; Score 51; DB 17; Length 298; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
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Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein (Fragment).
Hymo sapiens (Human)
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85.7%; Pred. No.
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TIGREAMS; TIGR01496; DHPS; 1.
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1-MAR-2002 (TrEMBLrel. 20,
1-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                 01-OCT-2003 (TrEMBLrel. 2
Dihydropteroate synthase.
PAE2937.
                                                                                                                                                                                                  PRELIMINARY;
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                     1 ILKKWPWWP
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TISSUE=Testis;
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Best Local Similarity
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SEQUENCE 298 AA;
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SEQUENCE
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Q9Y4N1 Q9Y4N1;

RESULT 13

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Search completed: May 4, 2004, 15:22:10 Job time : 35.886 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Мау Run on:

4, 2004, 15:08:11; Search time 45.7895 Seconds (without alignments) 74.047 Million cell updates/sec

US-09-444-281-36 86 Title: Perfect score: Sequence:

1 ILRWPWWPWRRK 12

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A_Geneseq_29Jan04:*
11. geneseqp1980s:*
22. geneseqp21980s:*
33. geneseqp2000s:*
43. geneseqp2001s:*
53. geneseqp2001s:*
64. geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARIES

		de			SUMMAKIES		
Result No.	Score	Query Match	Query Match Length	DB	ΙD	Description	
d	98	100.0	12		AAY24550		Indolicid
7	98	100.0	12	m	AAY94496	96	MBI-11B7
c	98	100.0	12	ო	AAY91791		o aci
4,	98	100.0	12	9	ADA00524	4	Antimicro
ស	86	100.0	12	7	ADC98871	Adc98871 Synt	Synthetic
9	86	100.0	12	7	ADC98903	Adc98903 Synt	Synthetic
7	86	100.0	14	7	ADC98990	Adc98990 Synt	Synthetic
œ	98	100.0	14	~	ADC98989	Adc98989 Synt	Synthetic
6	98	100.0	20	~	AAY24553		Indolicid
10	86	100.0	20	m	AAY91797	7	Amino aci
11	86	100.0	20	φ	ADA00530		Antimicro
15	98	100.0	20	۲	ADC98878	œ	Synthetic
13	98	100.0	21	7	AAW66376	Aaw66376 Cati	Cationic
14	98	100.0	21	~	AAY24554	-	Indolicid
15	98	100.0	21	(1	AAY24552	~	Indolicid
16	98	100.0	21	m	AAY91798	·	Amino aci
17	96	100.0	21	ო	AAY91796	Aay91796 Amino	o aci
18	98	100.0	21	φ	ADA00529		Antimicro
19	98	100.0	21	v	ADA00531	Ada00531 Anti	Antimicro
50	86	100.0	21	1	ADC98877	_	Synthetic
21	98	100.0	21	۲	ADC98879	Adc98879 Synt	Synthetic
22	98	100.0	27	N	AAW66363	~	Indolicid
23	98		28	m	AAY91800	Aay91800 Amino	o aci
24	98	100.0	28	9	ADA00533	~	Antimicro
25	96	100.0	28	7	ADC98881	Adc98881 Synt	Synthetic

	Aay91788 Amino aci	Ada00521 Antimicro	Adc98868 Synthetic	Aaw66364 Indolicid	4	Aay91817 Amino aci	Н	552	Ada00586 Antimicro	Adc98943 Synthetic	Adc98902 Synthetic	Aay24595 Indolicid	605	Aay91852 Amino aci		Ada00587 Antimicro	Ada00597 Antimicro	Adc98954 Synthetic	Adc98944 Synthetic
AAY24567	AAY91788	ADA00521	ADC98868	AAW66364	AAY24594	AAY91817	AAY91841	ADA00552	ADA00586	ADC98943	ADC98902	AAY24595	AAY24605	AAY91852	AAY91842	ADA00587	ADA00597	ADC98954	ADC98944
N	ო	ø	7	0	0	m	m	9	9	7	7	N	~	e	e	v	ø	7	7
12	12	12	12	12	12	12		12		12		12			12	12	12	12	12
		96.5		95.3		95.3	95.3	95.3	95.3	95.3			94.2			94.2			94.2
83	83	83	83	85	8	82	8	8	82	82	8	81	81	81	81	81	81	81	81
26	27	28	53	30	31	32	33	34		36			39	40	41	42	43	44	45

## ALIGNMENTS

AAY24550 standard; peptide; 12 AA. RESULT 1 AAY24550

(first entry) 18-AUG-1999

AAY24550;

Indolicidin analogue #2.

Indolicidin; bacterial infection; photo-oxidised solubiliser; autinicrobial; antibiotic; antiarrythmic; surface disinfectant; additive; shampoo; soap; insecticide; herbicide; preservative; food; technical material. 

Synthetic.

W09807745-A2

26-FEB-1998,

97WO-US014779. 21-AUG-1997;

96US-0024754P. 97US-0034949P. 21-AUG-1996; 13-JAN-1997; (MICR-) MICROLOGIX BIOTECH INC.

Taylor R, Erfle D; Fraser JR, West MH, Krieger TJ,

WPI; 1998-169090/15.

New indolicidin analogues with antimicrobial activity and related nucleic acid - vectors, transformed cells and antibodies, also conjugates with polyoxyalkylene glycol and fatty acid to reduce toxicity, useful therapeutically, as disinfectants etc.

Claim 11; Page 88; 129pp; English.

AAY24549 to AAY24615 represent indolicidin analogues of formulae (I)(VIII) containing up to 25 amino acids (aa): RXZXZXB (I), BXZXXZXB (II),
BBBZXXXXZB (III), BXZXXZXBBM(AA)nMILBBAGS (IV), BXZXXZXBB(AA)nM (V),
IBBRZXXXZXBK (VI), LKNXZXXZRBK (VII) and BBXZXXXZXBBB (VIII). Where Z = P or V; X = hydrophobic residue, preferably W; B = basic aa, preferably R
or K; AA = any aa; n = 0 or 1; in (II), at least 1 Z = V; in (VIII) at
least 2 X = F or Y. The analogues are used to treat infections caused by
bacteria (Gram positive or negative, or anaerobic); fungi (Yeast or
moulds); parasites (protozoa, nematodes, cestodes or trematodes) or

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viruses. Typical of very many pathogens that can be controlled are Leishmania, Trypanosoma, Ascaris lumbricoides, Fasciola hepatica, Katbasiella pneumoniae, Bordetella pertussis, Staphylococous aureus, Listeria, Clostridium, rotavirus and papilloma virus. Compounds derived from the analogues may be used similarly; the compounds may also be used therapeutically or to coat medical devices; also they are useful as surface disinfectants, as additives to shampoo or soaps, as insecticides or herbicides, or as preservatives for foods and technical materials. The analogues are administered by injection, lavage, orally or topically, generally at 0.1-50 mg/Kg. These analogues have a broader spectrum of activity than indolicidin and modification as compounds reduces their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain fusion protein expression cassette comprising a promoter and a nucleic acid molecule expressed as an insoluble protein. The inclusion of anionic peptide sequences in the linker sequences neutralises the positive charge of the cationic peptide so that the charge of the fusion protein is controlled. This cassette allows high yield, stable production of the cationic peptides such as bovine indolicidin may be used as antimicrobial agents. The present sequence is the MBI-11B7 peptide. MBI-11B7 is a cationic peptide derived from modifications of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cellulose binding domain; CBD; cationic peptide; MBI-11B7; indolicidin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A novel method allows the efficient production of cationic peptides in recombinant host cells. The method involves construction of a multi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Multi-domain fusion protein expression cassette used for high yield stable production of foreign peptide gene products.
                                                                                                                                                                                                                                                                                                                  100.0%; Score 86; DB 2; Length 12; 100.0%; Pred. No. 1.1e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MBI-11B7 peptide derived from indolicidin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 24; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY94496 standard; peptide; 12 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   1 ILRWPWWPWRRK 12
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                                                                                                                                                                                                                                                                                   Seguence 12 AA;
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                                                                                                                                                                                                                                            toxicity
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Sequence 12 AA;

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Gaps

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                                                                                                                                                                                                                                                                                  Cationic peptide, tumour; pharmaceutical composition; cancer; treatment; leukaemia; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma; breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel pharmaceutical composition containing optionally activated polyoxyalkylene-modified cationic peptides, useful for treating tumors.
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                               Gaps
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   Length 12;
                               Indels
                                                                                                                                                                                                                                                      Amino acid sequence of cationic peptide MBI 11B7CN
Score 86; DB 3; I
Pred. No. 1.1e-05;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADA00524 standard; peptide; 12 AA.
                                                                                                                                                                  AAY91791 standard; peptide; 12 AA.
   100.0%; Sc
100.0%; Pr
tive 0;
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Conservative C
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                                                                                                                                                                                                                              (first entry)
                                 Conservative
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                                                            1 ILRWPWWPWRRK 12
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                                                                                                                                                                                                                                                                                                                                    multidrug resistance
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                   Best Local Similarity
Matches 12; Conserv
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Best Local Simi
Matches 12;
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      Query Match
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01-JAN-2004 (first entry)
The present invention describes a composition (A) comprising an antimicrobial cationic peptide (I), a viscosity-increasing agent (II) and antimicrobial cationic peptide (I), a viscosity-increasing agent (II) and (III). (I) has antibacterial, virucide, antimifiammatory, (I), buffer (IV) and (III). (I) has antibacterial, virucide, antimifiammatory, fungicide, protozoscide, parasiticide, vulnerary, dermatological, (I) buffer (E) therbicide and insecticide activities. (A) can be used to reduce the population of microfilora (eukaryotes, proxaryotes or viruses) at a target site, particularly for treatment or prevention of infections. They can be used to treat a wide range of systemic infections (e.g. sepsis) and for topical treatment of wounds, but most especially can be used: (i) at sites where medical devices have been, or will be, inserted into the body (alternatively, they are used to treat the devices); and (ii) at sites on the skin (particularly for treating acne) or the mucosa. The devices treated are especially central venous, vascular dialysis, pulmonary or artery, peritornal dialysis or umbilical catheters. They may also be used as surface diainfectants; for treatment of clothing and air filters; in cometics and soaps; as herbicides and insecticides; in building materials (e.g. silicone sealants) and in processing animal products, e.g. hides. The present sequence respresence an antimitrobial actionic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Composition containing stabilized antimicrobial cationic protein, useful for treating infections, particularly where associated with in-dwelling
                                                                         antibacterial; virucide; antiinflammatory; fungicide; protozoacide; parasaiticide; vulnerary; dermatological; herbicide; insecticide; infection; systemic infection; sepsis; acne; disinfectant; herbicide; insecticide; silicone sealant.
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                                                          antimicrobial; cationic; viscosity-increasing agent; solvent; buffer;
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100.0%; Score 86; DB 6; Length 12
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels
                     Antimicrobial cationic peptide 11B7CN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fraser JR;
                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MICR-) MICROLOGIX BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                               2001US-0314232P.
2002US-00225087.
                                                                                                                                                                                                                                                                                                                                                                                        21-AUG-2002; 2002WO-US026525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Krieger TJ, Mcnicol PJ,
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Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                               21-AUG-2001;
20-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                 27-FEB-2003
                                                                                                                                                                                 Synthetic
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                                                 indolicidin analogue; antiseborrheic; dermatological; antiinflammatory; antiarthritic; immunosuppressive; vulnerary; antipruritic; antimicrobial; antipruritic; neuroprotective; antipsoriatic; inflammation; acne; arthritis; uctoimmune disease; burn; Crohn's; colitis; colitis; contact hypersensitivity; delayed; eczema; endotoxin shock syndrome; fibromyositis; graft rejection; microbial infection; multiple sclerosis; parapsoriasis; psoriasis; sclerosis; seborrhea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel indolicidin analog useful for treating or preventing inflammation at a target site associated with a condition such as acne, arthritis, burn, Crohn's disease, colitis, and in image analysis and diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 86; DB 7; L
100.0%; Pred. No. 1.1e-05;
ive 0; Mismatches 0;
Synthetic indolicidin analogue peptide - 1187CN.
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                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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26-AUG-2002; 2002US-00229368.
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les 12; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-AUG-2002; 2002WO-CA001351.
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RUBINCHIK E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-393247/37.
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                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
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                                                                                                                                                                                                                                                                                                                  Synthetic.
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(GUAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MICR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PAWL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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RESULT

ADC98871 standard; peptide; 12 AA.

ADC98871;

ADC98871 ID ADC9 XX AC ADC9 RESULT 5

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indolicidin analogue; antiseborrheic; dermatological; antiinflammatory; antiarthritic; immunosuppressive; vulnerary; antipruritic; antimicrobial; antipruritic; neuroprotective; antipsoriatic; inflammation; acne; arthritis; autoimmune disease; burn; Crohn's; colitis; cone; cone thypersensitivity; delayed; eczema; endotroxin shock syndrome; fibromyositis; graft rejection; microbial infection; multiple sclerosis; parapsoriasis; psoriasis; sclerosis; seborrhea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel indolicidin analog useful for treating or preventing inflammation at a target site associated with a condition such as acne, arthritis, burn, Crohn's disease, colitis, and in image analysis and diagnostic
                                                                      Synthetic indolicidin analogue peptide - R11B7 H CN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MICROLOGIX BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                            26-AUG-2002; 2002WO-CA001351.
                                                                                                                                                                                                                                                                                                                                                                                                        24-AUG-2001; 2001US-0315003P.
26-AUG-2002; 2002US-00229368.
                                           01-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mcnicol PJ, Pawlak SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MCNICOL P J.
PAWLAK S K.
RUBINCHIK E.
CAMERON D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-393247/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAMERON D.
GUARNA M M.
                                                                                                                                                                                                                                                                                                                  WO2003018619-A2.
                                                                                                                                                                                                                                                         Key
Modified-site
                                                                                                                                                                                                                                                                                                                                               06-MAR-2003
                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PAWL/)
(RUB1/)
(CAME/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MICR-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GUAR/)
The invention relates to a novel indolicidin analogue. The analogue of the invention demonstrates antisebornheic, dermatological, antiinflammatory, antiarthritic, immunosupressive, vulnerary, antipruritic, antimicrobial, antipruritic, neuroprotective and antiproxitic, antimicrobial, antipruritic, neuroprotective and at target site. The inflammation at the target site may be associated with a condition selected from acne, arthritis, autoimmune disease, burn, crohn's disease, colitis, contact hypersensitivity, delayed hypersensitivity, eczema, endotoxin shock syndrome, fibromyositis, graft rejection, microbial infection, multiple sclerosis, parapsoriasis, prespectasis, sclerosis and seborihea. The current sequence is that of the synthetic indolicidin analogue peptide of the invention.
                                                                                                                              indolicidin analogue, antieeborrheic, dermatological; antinflammatory, antiarthritic; immunosuppressive, vulnerary, antipruritic; antimicrobial; antipruritic; neuroprotective; antipsoriatic; inflammation; acne; arthritis; autoimmune disease; burn; Crohn's; colitis; colitis; contact hypersensitivity; delayed; eczema; endotoxin shock syndrome; fibromyositis; graft rejection; microbial infection; multiple sclerosis; parapsoriasis; sclerosis; seborrhea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel indolicidin analog useful for treating or preventing inflammation at a target site associated with a condition such as acne, arthritis, burn, Crohn's disease, colitis, and in image analysis and diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guarna MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 86; DB 7; Length 12; 100.0%; Pred. No. 1.1e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cameron D,
                                                                                                      Synthetic indolicidin analogue peptide - 11D21CN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rubinchik E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 48; 66pp; English.
                 ADC98903 standard, peptide, 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        (MICR-) MICROLOGIX BIOTECH INC. (RMCNI.) MONICOL P J. (PMRL) PMRLAK S K. (RUBI.) RUBINCHIK E.
                                                                                                                                                                                                                                                                                                                                                                              24-AUG-2001; 2001US-0315003P.
26-AUG-2002; 2002US-00229368.
                                                                                                                                                                                                                                                                                                                                                   26-AUG-2002; 2002WO-CA001351.
                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mcnicol PJ, Pawlak SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-393247/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GUARNA M M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12 AA;
                                                                                                                                                                                                                                                                                       WO2003018619-A2
                                                                           01-JAN-2004
                                                                                                                                                                                                                                                                                                                    06-MAR-2003
                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GUAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAME/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            assays.
 ADC98903
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Guarna MM;

Rubinchik E, Cameron D,

/note= "C-terminal amide" Location/Qualifiers 14

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                                              The invention relates to a novel indolicidin analogue. The analogue of the invention demonstrates antiseborrheic, dermatological, antisematory, antistribritio, immunosuppressive, vulnerary, antistribritio, antimucrobial, antipruritic, neuroprotective and antiproratic and may be useful for treating or preventing inflammation at a target site. The inflammation at the target site may be associated with a condition selected form acne, arthritis, autoimmune disease, burn, crohn's disease, colitis, contact hypersensitivity, delayed hypersensitivity, eczema, endotoxin shock syndrome, fibromyositis, prefection, microbial infection, multiple sclerosis, parapsoriasis, psoriasis, sclerosis and seborihea. The current sequence is that of the synthetic indolicidin analogue peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
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Example 1; Page 56; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ILRWPWWPWRRK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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ADC98990 standard; peptide; 14 AA.

RESULT 7 ADC98990

1 ILRWPWWPWRRK 12 ILRWPWWPWRRK 12

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ILRWPWWPWRRK

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Gaps

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RESULT 9

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antiarthritic; immunosuppressive; vulnerary; antipruritic; antimicrobial; antipruritic; neuroprotective; antiproratic; inflammation; acne; arthritis; autoimmune disease; burn; Crohn's; colitis; contact hypersensitivity; delayed; eczema; endotoxin shock syndrome; fibromyositis; graft rejection; microbial infection; multiple sclerosis; parapsoriasis; psoriasis; sclerosis; seborrhea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel indolicidin analogue. The analogue of antinflammatory, antiarthritic, immunosuppressive, vulnerary, antiarthritic, immunosuppressive, vulnerary, antipruritic, antimicrobial, antipruritic, neuroprotective and antipruritic, antimicrobial, artipruritic, neuroprotective and antiproriatic and may be useful for treating or preventing inflammation at the target site may be associated with a condition selected from acne, arthritis, autoimmune disease, burn, crohn's disease, colitis, contact hypersensitivity, delayed hypersensitivity, eczema, endotoxin shock syndrome, fibromyostis, purn, rejection, microbial infection, multiple sclerosis, parapsoriasis, psoriasis, psoriasis, clerosis and seborihea. The current sequence is that of the synthetic indolicidin analogue peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel indolicidin analog useful for treating or preventing inflammation at a target site associated with a condition such as acne, arthritis, burn, Crohn's disease, colitis, and in image analysis and diagnostic
                                                                                                                                                          indolicidin analogue; antiseborrheic; dermatological; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guarna MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 86; DB 7; Length 14; 100.0%; Pred. No. 1.3e-05; ive 0; Mismatches 0; Indels
                                                                                                                         Synthetic indolicidin analogue peptide - 11D21 CN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cameron
                                                                                                                                                                                                                                                                                                                                                                     /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rubinchik E,
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 56; 66pp; English.
                    ADC98989 standard; peptide; 14 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MICR-) MICROLOGIX BIOTECH INC. (MCNI/) MCNICOL P J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-AUG-2001; 2001US-0315003P.
26-AUG-2002; 2002US-00229368.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-AUG-2002; 2002WO-CA001351,
                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mcnicol PJ, Pawlak SK,
                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAWLAK S K.
RUBINCHIK E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-393247/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GUARNA M M.
                                                                                                                                                                                                                                                                                                                                                                                                        WO2003018619-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                        01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAR-2003
                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PAWL/) H
(RUBI/) H
(CAME/) C
(GUAR/) C
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ANY24549 to AAY24615 represent indolicidin analogues of formulae (I)-

(VIII) containing up to 25 amino acids (aa): RXZXXZBB (I), BXZXXZBB (II),

EBBRZXZXXZB (III), BXZXXZRBBM (VI), BXZXXZBB (AA) MM (V),

CLUBRAZZXXZBR (VI), LKANZXZXZRRR (VII) and BBYZXXXZBBB (VIII). Where Z LUBRAZZXXZRR (VII) and BBYZXXZXBBB (VIII). Where Z LUBRAZZAXZRR (VII) in (II), at least 1 Z = V; in (VIII) at least 2 X = V; in (VIII) at least 2 Z = V; in (VIII) at least 1 Z = V; in (VIII) at least 2 X = V; in CVIII) at least 3 X = V; in CVIII) at least 4 X = V; in CVIII) at least 5 X = V; in CVIII) at least 6 X = V; in CVIII) at least 6 X = V; in CVIII) at least 7 X = V; in CVIII) at least 8 X = V; in CVIII) at least 9 X = V; in CVIII at least 9 X = V; in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used therapeutically or to coat medical devices, also they are useful as surface disinfectants, as additives to shampoo or soaps, as insecticides or herbicides, or as preservatives for foods and technical materials. The
                                                                                                                                                                                                                           Indolicidin, bacterial infection, photo-oxidised solubiliser;
antinicrobial; antibiotic; antiarrythmic; surface disinfectant; additive;
shampoo, soap, insecticide; herbicide; preservative; food;
technical material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New indolicidin analogues with antimicrobial activity and related nucle acid - vectors, transformed cells and antibodies, also conjugates with polyoxyalkylene glycol and fatty acid to reduce toxicity, useful therapeutically, as disinfectants etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    analogues are administered by injection, lavage, orally or topically, generally at 0.1-50 mg/kg. These analogues have a broader spectrum of activity than indolicidin and modification as compounds reduces their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Erfle D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 86; DB 2; I 100.0%; Pred. No. 1.8e-05; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Taylor R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 West MH, Krieger TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 88; 129pp; English.
                   AAY24553 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MICR-) MICROLOGIX BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US014779.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0024754P.
97US-0034949P.
                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12
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                                                                                                                                                                          Indolicidin analogue #5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-169090/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                              WO9807745-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-1996;
13-JAN-1997;
                                                                                                                        18-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-1998,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fraser JR,
                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                          AAY24553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coxicity
AAY24553
                           쉱
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Gaps

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Local Similarity 100. nes 12; Conservative 1 ILRWPWWPWRRK 12 1 ILRWPWWPWRRK 12

Matches

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The present invention describes a composition (A) comprising an antimicrobial cationic peptide (I), a viscosity-increasing agent (II) and antimicrobial cationic peptide (I), a viscosity-increasing agent (II) and (III). Also described is a composition comprising (I), buffer (IV) and (III). (I) has antibacterial, virucide, antihifiammatory, buffer (IV) and (III). (I) has antibacterial, virucide, antihifiammatory, comparing insections entangency at the understy dermatological, composition of miscoflora (eukaryotes) prokaryotes or viruses) at a target comparing to treat a wide range of systemic infections (e.g. sepsis) and for composition of infections. They can be composed to treat a wide range of systemic infections (e.g. sepsis) and for compositions of wounds, but most especially can be used: (i) at sites where medical devices have been, or will be, inserted into the body composition (ii) at sites on the skin (particularly for treating acne) or the mucosa. The devices treated are especially central venous, vascular dialysis, pulmonary compositions and insecticides; in building compositions and in processing animal products; cometics and soaps; as herbicides and in processing animal products; composition, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                indolicidin analogue; antiseborrheic; dermatological; antiinflammatory; antiarthritic; immunosuppressive; vulnerary; antipruritic; antimicrobial; antipruritic; neuroprotective; antipsoriatic; inflammation; acne;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition containing stabilized antimicrobial cationic protein, useful for treating infections, particularly where associated with in-dwelling devices.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic indolicidin analogue peptide - 11B17CN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 86; DB 6; L
100.0%; Pred. No. 1.8e-05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                    Mcnicol PJ, Fraser JR;
                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC98878 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 47; 90pp; English.
                                                                                                           /label= amidated
                                                                                                                                                                                                                                                                                                                                                                     (MICR-) MICROLOGIX BIOTECH INC
                                                                                                                                                                                                                                                                                               21-AUG-2001; 2001US-0314232P.
20-AUG-2002; 2002US-00225087.
                                                                                                                                                                                                                                                    21-AUG-2002; 2002WO-US026525.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ILRWPWWPWRRK 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-332767/31
                                                                                                                                                        WO2003015809-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 AA;
                                                                     Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                    Krieger TJ,
                                                                                                                                                                                                          27-FEB-2003
                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC98878;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxyalkylene (APO) -modified cationic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with a multidrug resistant phenotype. The pharmaceutical composition can be used to treat tumours, specifically lymphoma, leukaenta, multiple myeloma, or tumours of breast, lung, ovary, cervix, uterus, skin, prostate, liver and colon
                                                                                                                                                                                                                                                         cancer; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel pharmaceutical composition containing optionally activated polyoxyalkylene-modified cationic peptides, useful for treating tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antimicrobial; cationic; viscosity-increasing agent; solvent; buffer; antibacterial; virucide; antiinflammatory; fungicide; protozoacide; parasticide; vulnerary; dermatological; herbicide; insecticide; infection; systemic infection; sepsis; acne; disinfectant; herbicide; insecticide; sealant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  West MHP;
                                                                                                                                                                                                                                                       Cationic peptide, tumour; pharmaceutical composition, cancer; treatmer
leukaemia; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma;
breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fraser JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                               Amino acid sequence of cationic peptide MBI 11B17CN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Erfle D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial cationic peptide 11B17CN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Taylor R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 15; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA00530 standard; peptide; 20 AA.
                                                                     AAY91797 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MICR-) MICROLOGIX BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-CA000552,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-00096541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                  multidrug resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-223549/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Friedland HD,
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14-JUN-1999; 12-JUN-1998;

23-DEC-1999

WO9965506-A2

Synthetic.

06-JUN-2000

AAY91797;

RESULT 10

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Gape ;

06-NOV-2003

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ADA00530;

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Length 20; Indels us-09-444-281-36.rag

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Sequence 21 AA;
                                                                                                                                                                 20-AUG-1997;
26-SEP-1997;
25-FEB-1998;
                        WO9840401-A2.
                                                                                                        10-MAR-1998;
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13-JAN-1997;
                                                                                                                                             10-MAR-1997;
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                                                                17-SEP-1998
                                                                                                                                                                                                                                                                                                Fraser JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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      %XCCCCCCCCCCX8X4444XX1X4XX1XX8X44X6X8X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel indolicidin analogue. The analogue of the invention demonstrates antiseborrheic, dermatological, antilificamatory, antiarthritic, immunosupressive, vulnerary, antipritarthritic, immunosupressive, vulnerary, antipritarthritic, antiprivitic, neuroprotective and antipropritic, antiprivitic, neuroprotective and antipropriatic and may be useful for treating or preventing inflammation at the target site may be associated with a condition selected from acne, arthritis, autoimmune disease, burn, crohn's disease, colitis, contact hypersensitivity, delayed hypersensitivity, eczema, endotoxin shock syndrome, fibromyositis, graft rejection, microbial infection, multiple sclerosis, parapsoriasis, periestion, aclerosis and seborrhea. The current sequence is that of the synthetic indolicidin analogue peptide of the invention.
             contact hypersensitivity; delayed; eczema; endotoxin shock syndrome; fibromyositis; graft rejection; microbial infection; multiple sclerosis; parapsoriasis; psoriasis; sclerosis; seborrhea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel indolicidin analog useful for treating or preventing inflammation at a target site associated with a condition such as acne, arthritis, burn, Crohn's disease, colitis, and in image analysis and diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indolicidin analogue; resistance; cationic peptide; antibiotic; bacteria; microorganism; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 86; DB 7; Length 20; 100.0%; Pred. No. 1.8e-05; ive 0; Mismatches 0; Indels
  arthritis; autoimmune disease; burn; Crohn's; colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cameron D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rubinchik E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 47; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW66376 standard; peptide; 21 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cationic peptide of claim 15 #3.
                                                                                                                                                                                                                                                                                                                                      MICROLOGIX BIOTECH INC.
                                                                                                                                                                                                                                                                     24-AUG-2001; 2001US-0315003P.
26-AUG-2002; 2002US-00229368.
                                                                                                                                                                                                                             26-AUG-2002; 2002WO-CA001351
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mcnicol PJ, Pawlak SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fungus; parasite; virus.
                                                                                                                                                                                                                                                                                                                                                              RUBINCHIK E.
CAMERON D
GUAPET
                                                                                                                                                                                                                                                                                                                                                     MCNICOL P J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-393247/37
                                                                                                                                             WO2003018619-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 AA;
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                                                                                                      Synthetic
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                                                                                                                                                                                                                                                                                                                                                                              (PAWL/)
(RUBI/)
(CAME/)
(GUAR/)
                                                                                                                                                                                                                                                                                                                                 (MICR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      assays.
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AAW66376
NAMES OF THE PROPERTY OF THE P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a specifically claimed cationic peptide from the present invention. The present invention describes compositions and methods for treating infection, sepecially bacterial infections. The compositions and methods use cationic peptides in combination with an antibiotic agent which are then administered to a patient to enhance the activity of the antibiotic agent, to overcome: (a) tolerance; (b) acquired resistance; and (c) inherent resistance. The combinations of antibiotics and cationic peptides can provide synergistic activity antibiotics and cationic poptides can provide synergistic activity against a microorganism that is tolerant, inherently resistant, or has acquired resistance to an antibiotic agent. They can be used for killing e.g. bacteria, fungi, parasites and viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                    New indolicidin peptide analogues - useful for, e.g. enhancing activity of antibiotic or overcoming tolerance, acquired resistance or inherent resistance of microorganisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 86; DB 2; Length 21
100.0%; Pred. No. 1.9e-05; Midmatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 15; Page 93; 105pp; English.
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                                                                                                                                                                                                                                                                                                           Mcnicol
                                                            97US-0040649P.
97US-00915314.
97US-0060099P.
98US-00030619.
                                                                                                                                                                                                                                       (MICR-) MICROLOGIX BIOTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0024754P.
97US-0034949P.
98WO-CA000190
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                       West MHP,
                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-520800/44.
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(MICR-) MICROLOGIX BIOTECH INC.
      WPI; 1998-169090/15
   Fraser JR,
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AAY24549 to AAY24615 represent indolicidin analogues of formulae (I)(VIII) containing up to 25 amino acids (aa): RXZXXXXB (I), BXZXXXXB (II),
BBRXZXXZXB (II), BXZXXZXBBBN (AA)nMILBBAGS (IV), BXZXXXXB (AA)
LBBRXZXXZXRK (VII), LKNZXXXXXRR (VII) and BRXZXXXXBB (AA)nM (V),
LBBRXZXXXXRK (VII), LKNZXXXXXRK (VII) and BRXZXXXXBB (AIII). Where Z

Or K; AA = any aa, n = 0 or 1; in (II), at least 1 = V; in (VIII) at

least 2 X = F or Y. The analogues are used to trematoficerably R

bacteria (Gram positive or negative, or anaerobic); fungi (yeast or

controlled are

leishmania, Trypanosoma, Accaris lumbricoides, Fasciola hepatica,

viruses. Typical of very many pathogens that can be controlled are

Leishmania, Trypanosoma, Accaris lumbricoides, Fasciola hepatica,

Klebsiella pneumoniae, Bordetella pertussis, Staphylococcus aureus,

Listeria, Clostridium, rotavirus and papilloma virus. Compounds derived

from the analogues may be used smilarly, the compounds may also be

prepared from antibiotics or antiarrythmic agents. The analogues may be

used therapeutically or to coat medical devices; also they are useful as

surface disinfectants, as additives to shampoo or soaps, as insecticides

or herbicides, or as preservatives for foods and technical materials. The

analogues are administered by injection, lavage, orally or topically,

generally at 0.1-50 mg/kg. These analogues have a broader spectrum of

activity than indolicidin and modification as compounds reduces their New indolicidin analogues with antimicrobial activity and related nucleic acid - vectors, transformed cells and antibodies, also conjugates with polyoxyalkylene glycol and fatty acid to reduce toxicity, useful therapeutically, as disinfectants etc. Claim 11; Page 88; 129pp; English Sequence 21 AA;

Local Similarity 100. Query Match Matches Best

100.0%; Score 86; DB 2; Length 21; 100.0%; Pred. No. 1.9e-05; tive 0; Mismatches 0; Indels

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AAY24552 standard; peptide; 21 AA. AAY24552

RESULT 15

18-AUG-1999 (first entry) AAY24552;

Indolicidin analogue #4.

Indolicidin, bacterial infection; photo-oxidised solubiliser; antimicrobial; antibictic; antiarrythmic; surface disinfectant; additive; shampoo; soap; insecticide; herbicide; preservative; food; technical material.

Synthetic.

WO9807745-A2

26-FEB-1998

97WO-US014779 21-AUG-1997;

21-AUG-1996; 13-JAN-1997 

96US-0024754P. 97US-0034949P.

(MICR-) MICROLOGIX BIOTECH INC.

Erfle Taylor R, Krieger TJ, West MH, Fraser JR,

Erfle D;

Taylor R,

Krieger IJ,

West MH,

'n

WPI; 1998-169090/15

New indolicidin analogues with antimicrobial activity and related nucleic acid - vectors, transformed cells and antibodies, also conjugates with polyoxyalkylene glycol and fatty acid to reduce toxicity, useful therapeutically, as disinfectants etc.

Claim 11, Page 88; 129pp; English.

AAY24549 to AAY24615 represent indolicidin analogues of formulae (1)(VIII) containing up to 25 amino acids (as): RXZXXXXB (1), BXZXXXXB (II),
BBAXXXXXXB (III), BXXXXXXBBBN (AA) MNILBBAGS (IV), BXZXXXXBB (AA) MN (V),
IBBNXAXXXXKK (VII), IKNXXXXXXRBN (VIII), Where Z =
C or K; AA = any as, n = 0 or 1; in (III), at least 1 Z = V; in (VIII) at
c or K; AA = any as, n = 0 or 1; in (III), at least 2 X = F or Y. The analogues are used to treat infections caused by
bacteria (Gram positive or negative, or anaerobic); fungi (yeast or
c moulds); parasites (protozoa, nematodes, cestodes or trematodes) or
c viruses. Typical of very many pathogens that can be controlled are
Leishmania Typical of very many pathogens that can be controlled are
Leishmania Typical of very many pathogens that can be controlled are
Leishmania Typical of very many pathogens that can be controlled are
Leishmania Typical of very many pathogens that can be controlled are
Leishmania Typical of very many pathogens that can be controlled are
Leishmania Typical of very many pathogens the compounds areas.

Klabsiella pneumoniae, Bordetella pertussis, Staphylococus aureus,
Listeria, Clostridium, rotavirus and papillome virus. Compounds derived
from the analogues may be used samilarly, the compounds may also be
prepared from antibiotics or antiarrythmic agents. The analogues may be
unface disinfectants, as additives to shampoo or soaps, as insecticides
or herbicides, or as preservatives for foods and technical materials.

C analogues are administered by injection, lavage, orally or topically,
c generally at 0.1-50 mg/Kg. These analogues have a broader spectrum of
activity than indolicidin and modification as compounds reduces their 

Sequence 21 AA;

toxicity

Gaps ö Length 21; Indels 100.0%; Score 86; DB 2; I 100.0%; Pred. No. 1.9e-05; iive 0; Mismatches 0; 12; Conservative Query Match Best Local Similarity Best Loca Matches

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/cgn2_6/ptddata/2/jaa/regrus_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Cuery Match
100.0%; Score 86; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 12; Conservative 0; Mismatches 0; Indels

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equence 78,		equence 83, equence 31, equence 40, equence 87, equence 83, equence 33, equence 38,		OR TREATING OF INDOLICIDIN ue	
8-915-314-7	US-08-915-314-85 US-08-915-314-86 US-09-030-619-83 US-09-030-619-89 US-09-667-486-78 US-09-667-486-85 US-09-667-486-86 US-09-667-486-86 US-09-667-486-86	08-915-314-8 09-030-619-3 09-030-619-8 09-030-67-486-8 09-667-486-8 09-667-486-8	ALIGNMENTS	R. H.P. H.P. H.P. SITIONS AND METHODS FOR TIONS USING ANALOGUES OF TIONS OF	
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. 00	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	800010W4R		RESULT 1  US-08-915-314-42  Sequence 42, Application Sequence 42, Application GENERAL INFORMATION: APPLICANT: Fraser, Ja APPLICANT: Krieger, To APPLICANT: Taylor, Ro TITLE OF INVENTION: I NUMBER OF SEQUENCES: COUNTRY: Seattle COUNTRY: Seattle COUNTRY: Washington COUNTRY: Washington COUNTRY: Readbable FORM MEDIUM TYPE: Floppy COMPUTER READBABLE FORM MEDIUM TYPE: PATCHION UNMBER: PILLING DATE: 20-AUG CLASSIFCATION: 44 ATTORNEY/AGENT INFORMA MANDE: REFERENCE/DOCKET NUM TELEPRAN: (206) 682- INFORMATION FOR SEQ ID N TYPE: ATTARET TO THE TYPE: TAY TYPE: ATTARET TO THE TYPE: TAY TO	- 00 -
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Sequence 47, Application US/08915314

Sequence 47, Application US/08915314

Sequence 47, Application

APPLICANT: Fraser, Janet R.

APPLICANT: TAYLOR, Robert

APPLICANT: TAYLOR, Robert

APPLICANT: TAYLOR, Robert

APPLICANT: Exfle, Douglas

TITLE OF INVENTION: COMPOSITIONS USING ANALOGUES OF INDOLICIDIN

TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN

WUMBER OF SEQUENCES: 90

CORRESPONDENCE ADDRESS:

ADDRESSES: SEED and BERRY LLP

ADDRESSES: SEED and BERRY LLP
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM Floppy disk
COMPUTER: IEM FC compatible
COMPUTER: PECPOS/MS-DOS
SOFTING SYSTEM: PC-DOS/MS-DOS
SOFTING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
FTLING DATE: 20-AUG-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 86; DB 3; I
100.0%; Pred. No. 4.4e-06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                    100.0%; Score 86; DB 4; 100.0%; Pred. No. 2.6e-06; iive 0; Mismatches 0;
                           660081.405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: No. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                             TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
REGISTRATION NUMBER: 39,317
REPERENCE/DOCKET NUMBER: 6600
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 aming acids
                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.0
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Best Local Similarity 100.
Matches 12, Conservative
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CITY: Seattle
STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
TOPOLOGY:
US-08-915-314-47
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                                                                                                                                                                                        APPLICANT: Exieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Taylor, Robert
APPLICANT: Exief, Douglas
APPLICANT: Exief, Douglas
APPLICANT: Exief, Douglas
APPLICANT: West, Michael H.P.
APPLICANT: West, Michael H.P.
APPLICANT: West, Michael H.P.
APPLICANT: West, Michael H.P.
TITLE OF INVENTION: WITH ANTIBIOTICS
TITLE OF INVENTION: WITH ANTIBIOTICS
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
CURRENT APPLICATION NUMBER: US/09/030,619B
NUMBER OF SEQ ID NGS: 232
SOFTWARE: FastSEQ for Windows Version 3.0
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Taylor, Robert
Erfle, Douglas
TILE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: LINFECTIONS USING ANALOGUES OF INDOLICIDIN
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/667,486

FILING DATA:

APPLICATION NUMBER: US/08/915,314

FILING DATA:

APPLICATION NUMBER: US/08/915,314

FILING DATA:

ATTORNEY/AGENT INFORMATION:

NAME: NO. 6538106tenburg Ph.D., Carol
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100.0%; Score 86; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 12; Conservative 0; Mismatches 0; Indels
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Indolicidin Analogue
0S-09-030-619-23
                                                                                                                         Sequence 23, Application US/09030619B Patent No. 6503881
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 42, Application US/09667486
Patent No. 6538106
GENERAL INFORMATION:
APPLICANT: Frager, Janet R.
West, Michael H.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 90
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STATE: Washington
COUNTRY: USA
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               1 ILRWPWWPWRRK 12
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LENGTH: 12
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Sequence 46, Application US/08915314

Patent No. 6180604

GENERAL INFORMATION:

APPLICANT: Fraser, Janet R.

APPLICANT: Krieger, Timothy J.

APPLICANT: Taylor, Robert

APPLICANT: APPLICANT: INPECTIONS USING ANALOGUES OF INDOLICIDIN

CORRESPONDENCE ADDRESS:

ADDRESSED: SEED and BERRY LLP

STATE: Washington

COMPUTRY: Seartle

COMPUTRY: USA

ZIP: 98104

COMPUTRY: USA
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Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                              Length 20;
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100.0%; Score 86; DB 4; I
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 12; Conservative 0; Mismatches 0;
                TELECOMPUNICATION INFORMATION:
TELEFRAX: (206) 622-4900
TELEFRAX: (206) 622-4900
TELEFRAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acide
TYPE: amino acide
STRANDEDRESS: cunknown>
TYPE: amino acid
STRANDEDRESS: cunknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
REGISTRATION NUMBER: 39,317
                                                                                                                                                                                                                                                                                                                                                                                                     1 ILRWPWWPWRRK 12
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US-08-915-314-46
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                                                                                                                                                                          APPLICANT: Rieger, Timothy J.
APPLICANT: Rajegr, Timothy J.
APPLICANT: Rajegr, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Taylor, Robert
APPLICANT: Fraser, Janet R.
APPLICANT: Praser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: Work Michael H.P.
APPLICANT: NUMBRIT APPLICATION UNMBRR: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBRR OF SEQ ID NOS: 232
SOFTWARE: FastSEQ for Windows Version 3.0
SSTORMARE: PastSEQ for Windows Version 3.0
SSTORMARE: PastSEQ for Windows Version 3.0
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Patent No. 6538106

GENERAL INFORMATION:
APPLICANT: Frase, Janet R.
Krieger, Timothy J.
Taylor, Robert
Erile, Douglast
Erile, Douglast
IITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: USDECTIONS USING ANALOGUES OF INDOLICIDIN
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100.0%; Score 86; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: FOCOMPUTER: IBM PC COMPUTER: IBM PC COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 22-Sep-2000
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 20-AUG-1997
ATTORNEY AGENT INFORMATION:
NAME: NO. 6538106tenburg Ph.D., Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Indolicidin Analogue US-09-030-619-24
                                                                                                            Sequence 24, Application US/09030619B Patent No. 6503881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
STATE: Washington
COUNTRY: USA
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       1 ILRWPWWPWRRK 12
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                                                                                              US-09-030-619-24
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APPLICANT: TAIGOET,
APPLICANT: TAIGOET,
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APPLICANT: TAIGOET,
APPLICANT: TAIGOET,
APPLICANT: TAIGOET,
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: WHITE OF INVENTION: WITH ANTIBIOTICS
FILE REPREMENCE: 660081.466
CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER: FastSEQ for Windows Version 3.0
SEQ ID NO 48
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fraser, Janet R.
West, Michael H.P.
West, Timothy J.
Taylor, Robert
Erfle, Douglas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: LIFECTIONS USING ANALOGUES OF INDOLICIDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
SIATE: Washington
                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 12; Conservative 0; Mismatches 0;
NUMBER OF SEQ ID NOS: 232
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 47
LENGTH: 21
                                                                                                            , OTHER INFORMATION: Indolicidin Analogue US-09-030-619-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Indolicidin Analogue
                                                                                                                                                                                                                                                                                                                                                                         Sequence 48, Application US/09030619B
Patent No. 6503881
GENERAL INFORMATION:
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Patent No. 6538106
GENERAL INFORMATION:
                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 90
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                                                                                                                                                                                                                                                                                                                                           RESULT 10
US-09-030-619-48
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Patent No. 650350...

APPLICANT: Krieger, Timothy J.

APPLICANT: Taylor, Robert

APPLICANT: Taylor, Robert

APPLICANT: Fraser, Janet R.

APPLICANT: West, Michael H.P.

TITLE OF INVENTION: WITH ANTIBLOTICS

TITLE OF INVENTION: WITH ANTIBLOTICS

FILE REFERENCE: 660081.406

CURRENT APPLICATION NUMBER: US/09/030,619B
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                                                     Ouery Match
Best Local Similarity 100.
Matches 12; Conservative
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       1 ILRWPWWPWRRK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-915-314-48
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Length 21; Indels ö

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GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Kriseger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Taylor, Robert
APPLICANT: Fraser, Janet R.
APPLICANT: Fraser, Janet R.
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: WINSTILON: OMBITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: WITH ANTIBIOTICS
TITLE OF INVENTION: WITH ANTIBIOTICS
TITLE OF INVENTION: WITH ANTIBIOTICS
TITLE OF INVENTION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO SO
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASPLICANT: Krieger, Timothy J.

APPLICANT: Taylor, Robert
APPLICANT: Taylor, Robert
APPLICANT: Taylor, Robert
APPLICANT: Frieser, Janet R.
APPLICANT: Frieser, Janet R.
APPLICANT: Praser, Janet R.
APPLICANT: Praser, Janet R.
APPLICANT: Monicol, Particia J.
APPLICANT: MINECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
ATTLE OF INVENTION: WITH ANTIBIOTICS
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Best Local Similarity 100.0%; Pred. No. 6.1e-06;
Matches 12; Conservative 0; Mismatches 0;
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: <Unknown>
JOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Indolicidin Analogue US-09-030-619-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 50, Application US/09030619B Patent No. 6503881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 12; Conservative
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| Patent No. 6538106
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| Rest, Michael H.P. |
| Krieger, Timothy J. |
| Taylor, Robert |
| Erfle, Douglas |
| Fifte OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
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EXTERNATION TYPE: FLORM:

MEDIUM TYPE: FLORM:

MEDIUM TYPE: FLORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APLICATION DATA:

APPLICATION NUMBER: US/09/667,486

FILING DATE: 22-Sep-2000

CLASSIFICATION: CURKNOWN>

PRIOR APPLICATION NUMBER: US/08/915,314

FILING DATE: 20-AUG-1997

ATTORNEY AGENT INFORMATION:

NAME: NO. 6538106tenburg Ph.D., Carol
                               COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/667,486

FILING DATE: 22-Sep-200

CLASSIFLATION NUMBER: US/08/915,314

APPLICATION NUMBER: US/08/915,314

FILING DATE: 20-AUG-1997

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 39,317

REGISTRATION NUMBER: 39,317

REGISTRATION NUMBER: 60081.405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 86; DB 4; Length 21; 100.0%; Pred. No. 4.6e-06; Live 0; Mismatches 0; Indels
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 46: US-09-667-486-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGIH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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US-09-667-486-48
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Sequence 40, Application US/08915314

Batent No. 6180604

GENERAL INFORMATION:
APPLICANT: Fraser, Janet R.
APPLICANT: Raser, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Taylor, Robert
APPLICANT: Taylor, Robert
APPLICANT: Erfle, Douglas
TITLE OF INVARION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEDD and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
STRY: Seattle
STRY: Seattle
COMURY: USA
ZIP: Machington
COUNTRY: USA
ZIP: PROPUTER: IEAD PO COMPACION:
COUNTRY: USA
COMPUTER: READBLE FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: READBLE FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: READBLE FORM:
MEDIUM TYPE: 20-AUG-1997
CILKING DATE: 20-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 99,317
REBERENCE/DOCKET NUMBER: 99,317
REMEMBRANCE/DOCKET NUMBER: 99,317
REMEMBRANCE/D
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Best Local Similarity 91.7%; Pred. No. 6.8e-06;
Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 6.1e-06;
Matches 12; Conservative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/09/030,619B CURRENT FILING DATE: 1998-02-25 NUMBER OF SEQ ID NOS: 232 SOFTWARE: PastSEQ for Windows Version 3.0 SEQ ID NO 104 LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                  , OTHER INFORMATION: Cationic Peptide Analogue US-09-030-619-104
                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ILRWPWWPWRRK 12
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TOPOLOGY: linear
US-08-915-314-40
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US-08-915-314-40
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Search completed: May 4, 2004, 15:23:52 Job time: 13.2632 secs
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Sequence 24, Appl
Sequence 30, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23, A Sequence 23, A Sequence 23, A Sequence 119, Sequence 60, A Sequence 60, A Sequence 63, A Sequence 42, A Sequence 42, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                             May 4, 2004, 15:22:18; Search time 34.4211 Seconds (without alignments) 96.635 Million cell updates/sec
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18: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-10-277-232-23

4 US-10-229-368-23

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4 US-10-229-087-119

US-10-395-896-60

US-10-395-896-68

US-10-395-896-68

US-10-395-896-68

US-10-395-896-68

US-10-395-896-69

US-10-395-896-69

US-10-377-233-23

US-10-277-233-23

US-10-277-232-24

US-10-277-232-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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               Copyright
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Match
                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                Scoring table:
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No.
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Sequence	Seducince		Sequenc	Sequenc	Seguen	Sequen	Seguence	Seguenc	Seguenc	Sequence	Seguen	Seguence	Sequence	Seguen	Sequence	Sequence	Seguen	Sequence	Sequenci	Sequence	Sequenc	Sequence	Sequenc	Sequence	Sequenc	Sequence	ĕ	Sequence		
10-225-087	TO-211-233-2	10-351-985-4	9-030-619-4	9-030-619-48	10-277-232-4	10-277-232-4	10-229-368-2	10-229-368-3	10-225-087-2	10-225-087-3	10-277-233-4	10-277-233-4	10-351-985-4	10-351-985-4	10-395-896-4	0-395-896-	10-395-896-4	10-395-896-5	10-395-896-5	10-395-896-5	10-395-896-5	10-395-896-5	10-395-896-5	-10-395-896-5	10-395-896-5	9-030-619-50	09-030-619-1	-10-277-232-5	-10-277-232-1	
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200	20	20	21	21	21	21	21	21	21	27	21	21	21	21	24	24	25	25	25	25	25	56	26	26	56	28	13 13	28	28	
0.00	90	00	80	00	00	00	00	00	00	00	00	90	00	00	00	00	00	00	00	00	00	00	00	00	90	80	ö	00	00	
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### ALIGNMENTS

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RESULT 1

US-09-030-619-23

US-09-010-623, Application US/09030619B

Patent No. US2002005061A1

GENERAL INFORMATION:

APPLICANT: Ridger, Timothy J.

APPLICANT: Tajlor, Robert

APPLICANT: Tajlor, Robert

APPLICANT: West, Machael H.P.

APPLICANT: Wollool, Patricia J.

ITILE OF INVENTION: UNIT ANTIBLOTICS

ITILE OF INVENTION: UNIT ANTIBLOTICS

ITILE OF INVENTION: UNIT ANTIBLOTICS

CURRENT FILEAD DATE: 1998-02-25

CURRENT FILEAD DATE: 1998-02-25

CURRENT FILEAD DATE: 1998-02-25

NUMBER OF SEQ ID NOS: 23

CURRENT FILEAD DATE: 1998-02-25

NUMBER OF SEQ ID NOS: 23

CURRENT FILEAD DATE: 1998-02-25

NUMBER OF SEQ ID NOS: 23

CURRENT SETURE: FastSEQ for Windows Version 3.0

SEQ ID NO 23

LENGTH: 12

CREATURE: FastSEQ for Windows Version 3.0

SEQ UD NO 23

CHER INFORMATION: Indolicidin Analogue

US-09-030-619-23

QUETY MACCH

Best Local Smilarity 100.0%; Pred. No. 0.00057;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gape 0;

ANTINE PROPERTY IL ILRWPWWWFRER 12

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RESULT 2 US-10-277-232-23

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 86; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels
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Publication No. US20030171281A1

GENERAL INFORMATION:
APPLICANT:
CURRENT PILING
APPLICATION UNMERR:
CURRENT PILING
APPLICANT:
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US-10-225-087-119
Sequence 119, Application US/10225087
Sequence 119, Application US/10225087
Dublication No. US20030171281A1
GENERAL INFORMATION:
APPLICANT: Krieger, Timothy J.
APPLICANT: Reser, Janet R.
TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES AND TITLE OF INVENTION: PORMULATIONS THEREOF;
FILE REFERENCE: 660081.417
CURRENT APPLICATION NUMBER: US/10/225,087
                                                                                                        APPLICANT: CMEETON, Dale
APPLICANT: Guarna, Maria Marta
APPLICANT: Guarna, Maria Marta
TITLE OF INVENTION: APMIMICROBIAL AND ANTI-INFLAMMATORY:
TITLE OF INVENTION: PEPTIDES
TITLE REPERENCE: 660081.418
CURRENT APPLICATION NUMBER: US/10/229,368
CURRENT APPLICATION NUMBER: 2002-08-26
NUMBER OF SEQ ID NOS: 140
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 55
LENGTH: 12
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100.0%; Score 86; DB 14;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Indolicidin peptide analogs US-10-229-368-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Indolicidin analog US-10-225-087-23
                   APPLICANT: McNicol, Patricia J.
                                                  Sonia K.
ik, Evelina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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                                                      Pawlak, Son
Rubinchik,
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                                                                                                                                                   APPLICANT: Taylor, Robert
APPLICANT: Faylor, Robert
APPLICANT: Erfle, Douglas
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: West, Michael H.P.
APPLICANT: MCN.col, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: WITH ANTIBIOTICS
TITLE OF INVENTION: WITH ANTIBIOTICS
TITLE OF INVENTION: WHERE LOSG.
CURRENT APPLICATION NUMBER: US.10/277,232
CURRENT FILING DATE: 2002-11-27
CURRENT FILING DATE: 2002-11-27
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 23
LENGTH: 12
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US-10-229-368-23
| Sequence 23, Application US/10229368 |
| Publication No. U220030148945A1 |
| GENERAL INFORMATION: Particia J. APPLICANT: MONICOL, Particia J. APPLICANT: Pawllak, Sonia K. APPLICANT: Pawllak, Sonia K. APPLICANT: Cameron, Dale APPLICANT: Cameron, Dale APPLICANT: Cameron, Dale APPLICANT: Cameron, Dale APPLICANT: Guarra, Maria Marta APPLICANT: WARTHAN PREPRIDES |
| TITLE OF INVENTION: APPLICATION NUMBER: US/10/229,368 |
| CURRENT PILING DAME: 2002-08-26 |
| NUMBER OF SEQ ID NOS: 140 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 2: 140 |
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Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0;
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OTHER INFORMATION: Indolicidin peptide analogs
US-10-229-368-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Indolicidin Analogue
Sequence 23, Application US/10277232
Publication No. US20030211537A1
GENERAL INFORMATION:
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                                                                                                                            APPLICANT: Krieger, Timothy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ILRWPWWPWRRK 12
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Sequence 55, Application US/10229368 Publication No. US20030148945A1 GENERAL INFORMATION:

US-10-229-368-55

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OTHER INFORMATION: Peptide formed during process for amidation of OTHER INFORMATION: 1187
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APPLICANT: Chen, Yuchen
APPLICANT: Chen, Yuchen
APPLICANT: Chen, Yuchen
APPLICANT: Chen, Yuchen
APPLICANT: Brinkman, Jacqui
APPLICANT: Brinkman, Jacqui
APPLICANT: Cabralda, Jennifer
APPLICANT: Metlitskaia, Luba
APPLICANT: SPORTION: ANTI-INFECTIVE PEPTIDES
TITLE OF INVENTION: ANTI-I
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100.0%; Score 86; DB 15;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OCHER INFORMATION: Indolicidin analouge 11B7CN
FBATURE:
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NAME: NOTE: NOTE: NAME: NOTE: NAME: NAME: NOTE: NOTE: NOTE: NOTE: NECESTRATION: Di-tert-butyl dicarbotate
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TITLE OF INVENTION: ANTI-INFECTIVE PEPTIDES FILE REFERENCE: 660081.421
CURRENT APPLICATION NUMBER: US/10/395,896
CURRENT FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 50
LENGTH: 12
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Best Local Similarity 100.
Matches 12; Conservative
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US-10-395-896-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 86; DB 14; Length 12; Best Local Similarity 100.0%; Pred. No. 0.00057; Matches 12; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: GUARTHA, MARTHA MARTHA
APPLICANT: CHEN, YUCHEN
APPLICANT: Chen, Yuchen
APPLICANT: Chen, Yuchen
APPLICANT: Carrinkman, Jacqui
APPLICANT: Cabraida, Jennifer
APPLICANT: Brinkman, Jacqui
APPLICANT: Mellitskaia, Luba
APPLICANT: MUNENTION: ANTI-INFECTIVE PEPTIDES
FILE REFERENCE: 660081.421
CURRENT APPLICATION NUMBER: US/10/395,896
CURRENT FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: LANDERS ANDERS AND
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Publication No. US20030219854A1
GENERAL INFORMATION:
APPLICANT: Guarna, Maria Marta
APPLICANT: Chen, Yuchen
APPLICANT: Carry, Robert
APPLICANT: Cabralda, Jennifer
APPLICANT: Brinkman, Jacqui
APPLICANT: Stilman, Jacqui
APPLICANT: Stilman, Dinar
APPLICANT: Stilman, Dinar
APPLICANS: Stilman, Dinar
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APPLICANS: Stilman, Dinar
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US-10-395-896-12
                                                                NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                              FEATURE:
OTHER INFORMATION: Indolicidin analog
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                       2003-01-10
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 12; Conservative
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                       CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-10-395-896-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-395-896-60
                                                                                                                                               SEQ ID NO 119
LENGTH: 12
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Gaps

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APPLICANT: Taylor, Robert
APPLICANT: Erfle, Douglas
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: Mondael H.P.
APPLICANT: Mondael H.P.
APPLICANT: Mondael H.P.
TILE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INPECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
                                                                                                                                                                                                                                                          ESULT 12

S-10-31-985-42

Sequence 42, Application US/10351985

Sequence 42.

GENERAL INFORMATION:

GENERAL INFORMATION:

Krieger, Timethy J.

Taylor, Robert

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING

TITLE OF INVENTION: OMPOSITIONS USING ANALOGUES OF INDOLICIDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Pepe, Jeff C.
REGISTRATION NUMBER: 46,985
REFERENCE/DOCKET NUMBER: 6600i
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 682-6931
INFORMATION FOR SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24, Application US/09030619B Patent No. US20020035061A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                            1 ILRWPWWPWRRK 12
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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| GENERAL INFORMATION: Timothy J. APPLICANT: Krieger. Timothy J. APPLICANT: Krieger. Timothy J. APPLICANT: Taylor, Robert
| APPLICANT: Taylor, Robert R. APPLICANT: Farser, Janet R. APPLICANT: Faster, Janet R. APPLICANT: Modical H.P. APPLICANT: Worklool) Patricial J. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
| TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION |
| TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION |
| TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION |
| TITLE OF INVENTION: 1006.11.06.01
| CURRENT APPLICATION NUMBER: US/10/277, 233 |
| CURRENT FILING DATE: 2002-10-18 |
| CURRENT FILING DATE: 2002-10-18 |
| SOFTWARE: FastESQ for Windows Version 3.0 |
| SEQ ID NO 23 |
| TENGTH: 12 |
| TYPE: RAT |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 86; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Di-tert-butyl dicarbonate and amidation US-10-395-896-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
Sequence 69, Application US/10395896
| Publication No. US20030219854A1
| Publication No. US20030219854A1
| APPLICANT Guarna, Maria Marta
| APPLICANT Chen, Yuchen
| APPLICANT Chen, Yuchen
| APPLICANT Brinkman, Jacqui
| APPLICANT Carbarla, Jennifer
| APPLICANT Suleman, Dinar APPLICANT SULEMANTON MANIT-INFECTIVE PEPTIDES
| TITLE OF INVENTION MANIT-INFECTIVE PEPTIDES
| TILLE REPERENCE: 660081.421 CURRENT APPLICANTON MOBBER: US/10/395,896 CURRENT PILING DATE: 2003-03-21 NUMBER OF SEQ ID NOS: 70 SOFUMARE: FastSEQ for Windows Version 4.0 SEQ ID NO SEQ 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION: Di-tert-butyl dicarbonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Indolicidin Analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23, Application US/10277233 Publication No. US20030232750A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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LOCATION: 1
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Sequence 24, Application US/10277232

Publication No. US20030211537A1

GENERAL INFORMATION: Timothy J.

APPLICANT: Trategr. Timothy J.

APPLICANT: Fraesr. Janet R.

APPLICANT: Fraesr. Janet R.

APPLICANT: West. Michael H.P.

APPLICANT: Wolical H.P.

APPLICANT: Wollow J.

TITLE OF INVENTION: WITH ANTIBIOTICS

FILE REFERENCE: 660081.40601

CURRENT APPLICATION NUMBER: US/10/277,232

CURRENT APPLICATION NUMBER: US/10/277,232

CURRENT APPLICATION NUMBER: US/10/277,232

CURRENT APPLIANG DATE: 2002-11-27

NUMBER OF SEQ ID NOS: 232

SECTIMARE: FESTESEQ for Windows Version 3.0

SEQ ID NO 24

LENTH: 20
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                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 86; DB 9; Length 20; Best Local Similarity 100.0%; Pred. No. 0.00085; Matches 12; Conservative 0; Mismatches 0; Indels
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Publication No. US20030146945A1
GENERAL INFORMATION:
APPLICANT: Pawlak, Sonia K.
APPLICANT: Rubinchik, Evelina
APPLICANT: Rubinchik, Evelina
APPLICANT: Guarna, Maria Marta
TITLE OF INVENTION: APPLIDES
TITLE OF INVENTION: PEPTIDES
FILE REFERENCE: 660001.418
CURRENT APPLICATION NUMBER: US/10/229,368
           FILE REFERENCE: 66001.406
CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SEQ ID NO 24
LENGTH: 20
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; OTHER INFORMATION: Indolicidin Analogue
US-10-277-232-24
                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Indolicidin Analogue US-09-030-619-24
WITH ANTIBIOTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ILRWPWWPWRRK 12
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TITLE OF INVENTION:
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US-10-277-232-24
                                                                                                                                                                                                                                                           FEATURE:
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

May 4, 2004, 15:15:37; Search time 11.0526 Seconds (without alignments) 104.437 Million cell updates/sec

US-09-444-281-36 86 Title: Perfect score: Sequence:

1 ILRWPWWPWRRK 12

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	indolicidin precur	E2 glycoprotein pr	hypothetical prote	hypothetical prote	protein F18G5.2 [i	ferredoxin-NADP re	hypothetical prote	conserved hypothet	NADH oxidase (H2O2	hypothetical prote	probable short-cha	Ĕ	ical	related to trfA pr	anthranilate synth	hypothetical prote	modulator of drug	monofunctional bio	probable MFS trans	щ	cyclic-nucleotide	ρι	yfrE protein - Yer	hypothetical prote	3-alpha-galactosyl	probable membrane	hypothetical prote	peplomeric polypro	
SUMMAKIES	QI	JC1222	VGIHHC	T12505	T29295	E89605	JT0751	T36208	AH0755	S23449	G70715	B83161	B70741	T48529	T51071	A39128	AC3353	S55483	F82646	A83604	H72376	A48508	AC1954	870177	B182	999	707	82	37	376
	ength DB	44	73	99	111 2	67	98	14	65	48	53	96	15	1411 2	28	05	87	96	73			80		57		61	97	35	. 12	30
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	Score	70	53	51	20	49	49	48.5	48	47	47	47	47	47	46	45.5	45	45	45	45	45	45	44	44	44	44	44		44	
	Result No.	; ; ; ;	7	m	4	r.	vo	7	æ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

RESULT 2
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	30	35 35	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 JC1222 indolicidin precursor - bovine	N,Alternate names: antimicrobial peptide C;Species: Bos primigenius taurus (cattle) C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999	Ridel Sal. G.; Storici, P.; Schneider, C.; Romeo, D.; Zanetti, M.	ArTitle cDNA cloning of the neutrophil bacteridal peptide indolicidin.	Ayracessince idulate: Octazz; Noib:2232300; Enibilatos; Ayracessince idulate: Octazz; Noib:2232300; AyMolecule type: mRNA	A; Residues: 1-144 <sal> A; Cross-references: EMBL:X67340; NID:g462; PIDN:CAA47755.1; PID:g463</sal>	A; Experimental source: bone marrow R; Selsted, M.E.; Jang, Y.Q.; Smith, W.; Cullor, J.S. R; Selsted, M.E.; Novotny, M.J.; Morris, W.L.; Tang, Y.Q.; Smith, W.; Cullor, J.S.	J. Biol. Chem. 267, 4292-4295, 1992  A.Title: Indolicidin, a novel bactericidal tridecapeptide amide from neutrophils.	A; Reference number: A42387; MUID:921657/1; PMiD:1537821 A; Accession: A42387	A:Molecule type: protein	A, Experimental source: neutrophils A. Note: semi-since extracted from NCBI backbone (NCBIP:83840)	C/Superfamily: cathelin; cystatin homology	C;Keywords: amidated carboxyl end F;1-29/Domain: signal sequence #status predicted <sig></sig>	F;22-129/Domain: cystatin homology <cys> F;30-130/Domain: propeptide #status predicted <pro></pro></cys>	Fill-143/Product: indolicidin #status experimental <mat> Fild3/Modified site: amidated carboxyl end (Arg) (amide in mature form from following</mat>	Ouery Match  Best Local Similarity 889.9%; Predo No. 0.014;  Dest Local Similarity 100 100 100 100 100 100 100 100 100 10	ימרדער די וודפוומרכזומם כי דיונפניזם כי כיניים	Qy 3 RWPWWFWRR 11	Db 135 KWPWWPWRR 143
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Gaps

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Indels

Length 111,

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A; Molecule type: DNA
A; Residues: 1-498 <TAK>
A; Residues: 1-498 <TAK>
A; Cross-references: GB:D83475; NID:g1199916; PIDN:BAA11921.1; PID:g4521308
A; Cross-references: GB:D83475; NID:g1199916; PIDN:BAA11921.1; PID:g4521308
A; Cross-references: GB:D83475; NID:g1199916; PIDN:BAA11921.1; PID:g4521308
A; Sagara, Y.; Takata, Y.; Miyata, T.; Hara, T.; Horiuchi, T.
J. Biochem: 102, 1333-1336, 1987
A; Title: Cloning and sequence analysis of adrenodoxin reductase cDNA from bovine adrena
A; Reference number: JT0079; MUID:88198050; PMID:3448086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rjanonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_el A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an A;Accession: E99605
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A;Residuse: 1-204.211-498 <8AG>
A;Residuse: 1-204.211-498 (190211) NID:G217433; PIDN:BAA00150.1; PID:G217434
A;Note: the deduced sequence is partially confirmed by amino acid sequencing of 15 isol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross_references: GB: chr_X; PIDN: AAA81082.1; PID: g1055093; GSPDB: GN00028; CESP: F18G5.
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C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Sate: 14-701-1994 #sequence_revision 18-0ct-1996 #text_change 03-Jun-2002
C;Accession: JT0751; JT0079; JS3390; S03588; P60003; A29604; S22100
R;Takata, Y; Sagara, Y; Kono, A.; Sekimizu, K.; Horiuchi, T.
Biol. Pharm. Bull. 16, 1200-1206, 1993
A;Title: Gene structure of bovine adrenodoxin reductase.
A;Reference number: JT0751; MUID:94177140; PMID:8130767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein F18G5.2 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
C;Accession: E86605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ferredoxin-NADP reductase (EC 1.18.1.2), long form precursor - bovine
A;Cross-references: EMBL:U41557; PIDN:AAA83303.1; CESP:C50F7.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Segara, Y.
submitted to DDBJ, September 1989
A;Reference number: JS0390
A;Contents: revision, insertion of residues 205-210
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Pred. No. 22;
0; Mismatches
                                                                                                                                                          Score 50; DB 2
Pred. No. 4.1;
2; Mismatches
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ilarity 54.5%;
Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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Matches 6; Conserv
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A;Molecule type: DNA
                                                      C;Genetics:
A;Gene: CESP:C50F7.8
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                                                                      A/Recession: A34766

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A/Recession: A34766

A/Recession: A34766

A/Residues: 1-173 -RAA>

A/Cross-references: EMBL:X16816; NID:g58926; PIDN:CAA34723.1; PID:g58927

A/Experimental Source: strain 229E

R/Rabe, T.; Siddell, S.
Nucleic Acids Res. 17, 6387, 1989

A/Title: Nucleotide sequence of the human coronavirus HCV 229E mRNA 4 and mRNA 5 unique

A/Reference number: A34038; MUID:8936667; PMID:2701946

A/Recession: S05460

A/Rocession: S05460

A/Residues: 1159-1173 -RA2>

A/Rocession: S159-1173 -RA2>

A/Residues: 1159-1173 -RA3>

A/Residue
    A;Title: Nucleotide sequence of the gene encoding the spike glycoprotein of human corona A;Reference number: A34766; MUID:90264837; PMID:2345367 A;Accession: A34766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Mixturer, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. Siansorge, W.; Mixturer, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. Submitted to the Protein Sequence Database, June 1999
A; Reference number: Z17527
A; Reference trype: many
A; Residues: T12505
A; Status: preliminary
A; Residues: 1-299 < ANS
A; Residues: 1-299 < ANS
A; Cross-references: EMBL: AL096753
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Pred. No. 7.9;
0; Mismatches 1
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Best Local Similarity 85.7%;
Matches 6; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
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Gaps

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Indels

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Length 467;

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G;Accession: AH0755
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher Pt. T.; Connexton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K. A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein STY2208 [imported] - Salmonella enterica subsp. enterica C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the gene encoding a H(2)O(2)-form
                      PIDN: CAB42078.1; GSPDB:GN00070; SCOEDB:SCE36.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Cross-references: GB:AL513382; PIDN:CAD05747.1; PID:g16503239; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Species: Thermus aquaticus
C,Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 30-Sep-2002
C,Accession: S23449; S24556
                                                                                                                                                                                                                                   ä
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                                                                                                                                                                            Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R.Park, H.J.; Kreutzer, R.; Reiser, C.O.A.; Sprinzl, M. Eur. J. Blochem. 205, 875-879, 1992.
A.Title: Molecular cloning and nucleotide sequence of the Askeference number: S23449; MUID:92249331; PMID:1577004.
A.Accession: S23449
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Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                         Score 48.5; DB
Pred. No. 6.6;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.8%; Score 48; DB
larity 31.6%; Pred. No. 17;
Conservative 3; Mismatches
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                         A,Cross-references: EMBL:AL049763;
A,Experimental source: strain A3(2)
C,Genetics:
A,Gene: SCOEDB:SCE36.09
                                                                                                                                                                      56.4%;
ilarity 80.0%;
Conservative
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A;Residues: 1-248 <PAR>
A;Cross-references: EMBL:X60110
A;Accession: S24556
                                                                                                                                                                                                                                                                                                                                                         103 RWRPRWPWRR 112
                                                                                                                                                                                                                                                                                                3 RW-PWWPWRR 11
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Matches 6; Conserv
                                                                                                                                                                                                      Best Local Similarity
Matches 8; Conserv
A;Residues: 1-114 <OLI>
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A;Status: preliminary
A;Molecule type: DNA
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      A.Moceosian. 16499 - 622.7

A.Moceosian. 16499 - 622.7

A.Moceosian. 16499 - 622.7

A.Moceosian. 16499 - 622.7

A.Moceosian. 16499 - 622.7

A.Moceosian. 16499 - 622.7

A.Moceosian. 16499 - 622.7

A.Moceosian. 16499 - 622.8

A.
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C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: 176208
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, May 1999
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A;Accession: T36208
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Accession: JS0390
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Matches 5
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Telated to triA protein [imported] - Neurospora crassa

N,Alternate names: protein B2A19.50

C;Species: Neurospora crassa

C;Species: Neurospora crassa

C;Date: 21-Uul-2000 #sequence_revision 21-Uul-2000 #text_change 21-Uul-2000

C;Accession: T51071

R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura submitted to the Protein Sequence Database, July 2000

A;Reference number: Z25286

A;Accession: T51071
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C; Accession: B70741
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Anthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whithehead, S.; Barrell, B.G. A; Reference number: Sqares, R.; Sulston, J.E.; Taylor, K.; Whithehead, S.; Barrell, B.G. A; Reference number: A70500; MUD: 98295987; PMID: 9634230
A; Accession: B70741
A; Accession: B70741
A; Residues: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule trye: DNA
A; Residues: 1-715 < COL>
A; Residues: 1-715 < COL>
A; Residues: 1-715 < COL>
A; Experimental source: strain H37Rv
C; Genetics:
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A,Introns: 281/2; 320/1; 389/3; 429/3; 473/3; 515/3; 534/2; 567/3; 602/1; 669/1; 776/2;
A,Note: T22P22.90
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R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft submitted to the Protein Sequence Database, April 2000
A;Reference number: 224490
A;Accession: T48529
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
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A;Molecule type: DNA
A;Residues: 1-728 <SCH>
A;Cross_references: EMBL;AL390092; GSPDB:GN00116; NCSP:B2A19.50
A;Experimental source: BAC clone B2A19; strain OR74A
C;Genetics:
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A;Molecule type: DNA
A;Rosidues: 1-1411 <BEV>
A;Cross-references: EMBL:All63814
A;Experimental source: cultivar Columbia; BAC clone T22P22
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Pred. No. 59;
2; Mismatches
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ilarity 66.7%;
Conservative
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Best Local Similarity
6, Conserve
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RWAYYPWRR
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Matches 7; Conserv
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C; pecies: Mycobacterium tuberculosis
C; pecies: Mycobacterium tuberculosis
C; pecies: Mycobacterium tuberculosis
C; pecies: Mycobacterium tuberculosis
C; Accession: Globb, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70800; MuID: 98295987; PMID: 9634230
A; Reference number: A70800; MuID: 98295987; PMID: 9634230
A; Accession: G70715
A; Residues: 1-253 «COL»
A; Residues: 1-253 «COL»
A; Residues: 1-253 «COL»
A; Residues: 1-253 «COL»
A; Resperimental source: Strain H37Rv
C; Genetics:
A; Genetics:
A; Genetics: Rv0945
C; Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
F; 8-190/Domain: short-chain alcohol dehydrogenase homology
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B31461
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, ature 406, 959-964, 2000
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Accession: B83161
A Status: preliminary
A Molecule type: him ary
A; Residues: 1-276 <STO>
A; Cross-references: GB: AE004805; GB: AE004091; NID: g9950055; PIDN: AAG07270.1; GSPDB: GN001
A; Experimental source: strain PAO1
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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hypothetical protein Rv0945 - Mycobacterium currely hypothetical protein Rv0945 - Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: 17-Uul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Date: 17-Uul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Date: 17-Uul-1998 #sequence_revision 17-Jul-1998 #text_change Northery Norther
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C;Species: Mycobacterium tuberculosis
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54.7%; Score 47; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
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Pred. No. 24;
1; Mismatches
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70.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
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Gaps

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RESULT 15
anthranilate synthase (EC 4.1.3.27) component I (validated) - Pseudomonas syringae pv. 8
Anthranilate synthase alpha chain
N.Alternate names: anthranilate synthase alpha chain
C.Species: Pseudomonas syringae pv. savastanoi
C.Species: Bseudomonas syringae pv. savastanoi
C.Species: Davar-2000
C.Saccesion: A39128
R.da Costa, E.; Sllva, O.; Kosuge, T.
A.Title: Molecular characterization and expression analysis of the anthranilate synthase
A.Reference number: A39128; MUD:91100331; PMID:1987141
A.Reference number: A39128
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-505 < DAC>
A.Ganetics:
C.Genetics:
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CComplex: heterotetramer; two component I chains, two component II chains
Cjouncion: ANT>
AjDescription: EC 4.1.3.27 [validated, MUID:90130325]
AjDescription: EC 4.1.3.27 [validated, MUID:9110033]
Cjeunction: AjDescription: EC 4.1.3.27 [validated, MUID:9110033]
Cjeunction: AjDescription: EC 4.1.3.27 [validated, MUID:9110033]
Cjeunction: Addition: EC 4.1.3.27 [validated, MUID:9110033]
Cjeunction: EC 4.1.3.27 [validated, M
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                                                                                                                                                                                                                                           Query Match 53.5%; Score 46; DB 2; Length 728; Best Local Similarity 58.3%; Pred. No. 81; Matches 7; Conservative 1; Mismatches 4; Indels
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Best Local Similarity 28.0%; Pred. No. 66;
Matches 7; Conservative 2; Mismatches
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A,Gene: NCSP:B2A19.50
A,Map position: 6
A,Introns: 26/1; 119/2
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Search completed: May 4, 2004, 15:22:59 Job time: 12.0526 secs

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GenCore version 5.1.6
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                  Copyright
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protein search, using sw model ı OM protein Мау Run on:

4, 2004, 15:08:51 ; Search time 7.57895 Seconds (without alignments) 82.444 Million cell updates/sec

US-09-444-281-36 86

1 ILRWPWWPWRRK 12 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### STEMMARTES

		Description	ĝ	P15423 human coron	Q96119 homo sapien		P71564 mycobacteri				ratt		pan					mus mu	avian		avian	avian	-									mycob	70 homo sapie	555 porci	413
SUMMARIES		σī	INDC BOVIN	VGL2_CVH22	WS18 HUMAN	ADRO_BOVIN	Y945 MYCTU	YD55_MYCTU	TRPE_PSESS	YA05_SCHPO	CN3B_RAT	FUT3_HUMAN	FUT3_PANTR	MML6_MYCTU	YDW6_SCHPO	MML4_MYCTU	MML2_MYCTU	SX13_MOUSE	VGL2_IBVD2	VGL2_IBVB	VGL2_IBVK	VGL2_IBVM	VGL2_IBV6	VGL2_CVHSA	RCEL_RHOPA	ABC2_HUMAN	LHB2_ECTHA	NPD1_PSEAE		NPD4_PSESM		MML1_MYCTU		VGL2_CVPR8	VGL2_CVPRM
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P11225 murine coro	PIIZZ4 murine coro P36334 human coron	P25190 bovine coro	P25191 bovine coro	P25192 bovine coro	P15777 bovine coro	P25193 bovine coro	P25194 bovine coro	P22432 murine coro	Q02385 murine coro	P07946 porcine tra	
VGL2_CVMJH	VGL2_CVMA5	VGL2_CVBF	VGL2_CVBL9	VGL2_CVBLY	VGL2_CVBM	VGL2_CVBQ	VGL2_CVBV	VGL2 CVM4	VGL2 CVMJC	VGL2_CVPPU	
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### ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Bone marrow;
MEDLINE-92392368; PubMed=1520337;
del Sal G., Storici P., Schneider C., Romeo D., Zanetti M.;
"CDMA cloning of the neutrophil bactericidal peptide indolicidin.";
Biochem. Biophys. Res. Commun. 187:467-472(1992).
                                       01-00T-1993 (Rel. 27, Created)
01-00T-1993 (Rel. 27, Last sequence update)
10-00T-2003 (Rel. 42, Last annotation update)
10-00T-2003 (Rel. 42, Last annotation update)
Bos taurus (Bovine).
Busaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bovidae; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
NOBL_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DR PIR; JC1222; JC1222.
DR PIB; JG89; 17-JAN-01.
DR PDB; 1G80; 17-JAN-01.
DR PDB; HRI; 31-DEC-02.
DR PDB; HRI; Anteloidins.
DR PCOSTE; PS00946; CATHELICIDINS_1; 1.
DR PROSITE; PS00947; CATHELICIDINS_1; 1.
DR PROSITE; PS00947; CATHELICIDINS_2; 1.
DR PROSITE; PS00947; CATHELICIDINS_1; 1.
DR PDB; PDB; PS00947; CATHELICIDINS_1; 1.
DR PROSITE; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Neutrophils;
MEDLINE=92165771; PubMed=1537821;
Selsted M.E., Novotny M.J., Morris W.L., Tang Y.-Q., Smith W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cullor J.S.;
"Indolicidin, a novel bactericidal tridecapeptide amide from neutrophila."
15 Biol. Chem. 267:4292-4295(1992).
1- FINCTION: Pocent microbicidal activity, active against Staphylococus aureus and Escherichia coli.
1- TISSUE SPECIFFITY: Large granules of neutrophils.
1- TISSUE SPECIFFITY: Large granules of neutrophils.
1- PIN: Elastase might be responsible for its maturation.
1- SIMILARITY: Belongs to the cathelicidin family.
                                   PRT;
                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 131-143.
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                   BOVIN
BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1159-1173 FROM N.A.
MEDILINES89366667; PubMed=2701946;
Raabe T., Siddell S.;
"Nucleotide sequence of the human coronavirus HCV 229E mRNA 4 and mRNA
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE PROM N.A.
MEDLINE=90264837; PubMed=2345367;
Raabe T., Schelle-Prinz B., Siddell S.G.;
"Nucleotide sequence of the gene encoding the spike glycoprotein of human coronavirus HVV 229E.";
J. Gen. Virol. 71:1065-1073(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=21262210; PubMed=11369870;
Thiel V., Herold J., Schelle B., Siddell S.G.;
"Infectious RNA transcribed in vitro from a cDNA copy of the human coronavirus genome cloned in vaccinia virus.";
                           PYRECLIDORE CARBOXYLIC ACID (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
AMIDATION (G-144 PROVIDE AMIDE GROUP).
E3BICBBE55C09911 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           Human coronavirus (atrain 229E) (HCOV-229E).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERACTION WITH ANPEP.
MEDLINE=22440020; PubMed=12551991;
Bonavia A., Zelus B.D., Wentworth D.E., Talbot P.J., Holmes K.V.;
                                                                                                                                                                                                                                                                                                                                                                                                 (Peplomer protein)
                                                                                                                                                                                                                                                                                                          VGL2_CVH22 STANDARD; PRT; 1173 AA.
P15423; P89342; P89343; P89344; Q66174; Q990M1; Q990M2; Q990M3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 98-1113 FROM N.A., AND VARIANTS.
STRAID=ISOLAGATE ATCC VR-74, ISOLAGE A162, and ISOLAGE LRI 281;
MEDLINE=999086149;
PHAYS J.P., Myint S.H.;
HAYS SEQUENCING Of the spike genes of geographically and chronologically distinct human coconaviruses 229E.";
J. Virol. Methods 75:179-193 (1998).
                                                                                                                                  Score 70; DB 1; Length 144;
Pred. No. 0.0068;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [3]
SEGUENCE OF 98-1113 FROM N.A., AND VARIANTS.
STRAIN-ISCIATE RW STOCK, ISCIATE P100E, ISCIATE P11A, and
ISCIATE P11B;
                                                                                                                                                                                                                                                                                                                                                                                                   E2 glycoprotein precursor (Spike glycoprotein)
                                                                                                                                                                                                                                                                                                                                                  01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 unique regions.";
Nucleic Acids Res. 17:6387-6387(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gen. Virol. 82:1273-1281(2001).
                                                                                                          MM;
                                                                                                                                     81.4%;
                                                                                                                                                    88.98;
                                                                                                                    Query Match
Best Local Similarity 88.3°,
Best Local Similarity 88.3°,
                                                                                                          16479
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124
143
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135 KWPWWPWRR 143
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                                                                                                        144 AA;
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MOD_RES
SEQUENCE
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MOD_RES
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VGL2 CVH22
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                                                                                                                                                                                                                                   MEDIINE=21109095; PubMed=11162792;

Gallagher T.M., Buchmeier M.J.;

Gallagher T.M., Buchmeier M.J.;

Gology 279:371-374(2001).

'Coronavirus spike proteins in viral entry and pathogenesis.";

Virology 279:371-374(2001).

'I FUNCTION: Structural protein that makes spikes at the surface of the virus. Determines enteropathogenicity and virulence of the virus. Initiates infection by specifically recognizing and binding the human aminopeptidase ANPEP receptor. Its association with ANPEP may lead to its conformational change that triggers fusion between viral and host cellular membrane.

-!- SUBUNI: Homotriner. During virus morphogenesis, it is found in a complex with M and HE proteins (By similarity). Interacts with
"Identification of a receptor-binding domain of the spike glycoprotein of human coronavirus HCOV-229E.", J. virol. 77:2530-2538(2003).
                                                                         INTERACTION WITH ANPED.

MEDLINES2221443; PubMed=12634402;

MEDLINES222143; PubMed=12634402;

Brealin J.J., Mork P.J., Shoetrom H., Noren O., Holmes K.V.;

Bonavia A., Talbot P.J., Sjoestrom H., Noren O., Holmes K.V.;

"Human cocronavirus 2258: receptor binding domain and neutralization by soluble receptor at 37 degrees C.";

J. Virol. 77:4435-4438(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor.

-!- DOMAIN: The leucine zipper-like heptad repeats may mediate the fusion of viral and cellular membranes.
-!- POLYMORPHISM: The strong variation between the different strains may affect the virulence of the virus.
-!- MISCELLANBOUS: In contrast to serogroup 2, E2 glycoprotein protein from serogroup 1 is not cleaved.
-!- SIMILARITY: Contains 1 spike S1 domain.
-!- SIMILARITY: Contains 1 spike S2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- DOMAIN: The spike S1 domain displays the specificity for the host
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AF344186; AAK32188.1;
AF344187; AAK32189.1;
AF44188; AAK32190.1;
AF344189; AAK32190.1;
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InterPro; IPR002552; Corona_S2.
Pfam; PF01600; Corona_S1; I.
Pfam; PF01601; Corona_S2; 1.
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EMBL; Y10051; CAA71146.1; -..
EMBL; Y10052; CAA71147.1; -..
EMBL; X1654; CAA33680.1; -..
PIR; A34766; VGIHHC.
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Coiled coil.
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WS18_HUMAN
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KYVAVYANVG -> QFVGAKFD (in isolate A162).

WAYSKYT -> LANLNSHN (in isolate A162).

S -> T (in isolate A162).

Q -> K (in isolate A162).

V -> A (in isolate A162).

V -> N (in isolate A162).

L -> V (in isolate A162).

T -> I (in isolate P118).

Y -> G (in isolate P118).

Y -> G (in isolate P118).

T -> I (in isolate P108).

T -> R (in isolate A162).

L -> I (in isolate A162).
                                                                                                                                                                                                                                                                                                                                                                   N -> S (in isolate LRI 281).

N -> I (in isolate LRI 281).

LR -> IS (in isolate LRI 281).

N -> T (in isolate A162).

T -> S (in isolate A162).

T -> N (in isolate A162).

C -> L (in isolate A162).

C -> F (in isolate A162).

C -> F (in isolate LRI 281).

N -> A (in isolate LRI 281).

N -> A (in isolate LRI 281).

T -> M (in isolate LRI 281).

T -> M (in isolate A162).

PQ -> LR (in isolate A162).
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-> N (in isolates RW Stock,
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TESUBLEAURY,

RA MEDDINE=2238857; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altaner R.D., Collins F.S., Wagner L., Sheamen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Butcow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Butcow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg M.B., Pornet T., Mang J., Heieh F.,

RA Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

RA Bata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., NcEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.F.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Norley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Generation and initial analysis of more than 15,000 full-length

RT "Generation and initial analysis of more than 15,000 full-length

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

LTISSUB SPECIFICITY: Expressed in brain, heart, kidney, liver,

L. TISSUB Specific Expressed in brain, heart, kidney, liver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lung, spleen, stomach and testis.

-i- DISEASE: Haploinsufficiency of WBSCR18 may be the cause of certain cardiovascular and musculo-skeletal abnormalities observed in Williams-Beuren syndrome (WBS), a rare developmental disorder. It is a contiguous gene deletion syndrome involving genes from chromosome band 7q11.23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Testis;
Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y., Ishibashi T., Kanehori K., Takiguchi S., Kusano J., Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita F., Chiba Y., Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B., Nagai K., Isogai T., Sugio project.";
"NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=22067697; PubMed=12073013;
Merla G., Ucla C., Guipponi M., Reymond A.;
"Identification of additional transcripts in the Williams-Beuren syndrome critical region.";
Hum. Genet. 110:429-438(2002).
                                                                                                                                                                                           .
0
                                                                                           Length 1173,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WS18 HUMAN STANDARD; PRT; 226 AA.
Q96LL5; Q9BSG8;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Williams-Beuren syndrome chromosome region 18 protein.
A -> S (in isolate A162)
                                                                                           Score 53; DB 1;
Pred. No. 7.5;
2; Mismatches
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                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=87270696; PubMed=3038094;
Nonaka Y., Murakami H., Yabusaki Y., Kuramitsu S., Kagamiyama H.,
Nonaka Y., Okamoto M.;
"Molecular Cloning and sequence analysis of full-length cDNA for mRNA
of adrenodoxin oxidoreductase from bovine adrenal cortex.";
[4]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
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P08155; QSPAN8;
01-AUG-1988 [Rel. 08, Created)
15-UL-1998 [Rel. 36, Last sequence update)
15-UMR-2004 [Rel. 43, Last annotation update)
15-MAR-2004 [Rel. 43, Last annotation update)
16-MAR-2004 [Rel. 40]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.0%; Score 49; DB 1; Length 226;
llarity 53.8%; Pred. No. 5.2;
Conservative 1; Mismatches 1; Indels
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SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=94177140; PubMed=8130767;
Takata Y., Sagara Y., Kono A., Sekimizu K., Horiuchi T.;
"Gene structure of bovine adrenodoxin reductase.";
Biol. Pharm. Bull. 16:1200-1206(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       J-DOMAIN.
G -> R (IN REF. 3).
; 8687C2A45790381D CRC64;
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MEDLINE=88198050; PubMed=3448086;
                                                                                                                                                                                                                                                                                                                           Pfan: PF00226; DnaJ; 1.
PRINTS; PR00625; DNaJPROTEIN.
SMART; SM00271; DnaJ; 1.
PROSITE; PS00636; DNAJ 1; FALSE_NEG.
PROSITE; PS50076; DNAJ 2; 1.
Chaperone; Williams-Beuren syndrome.
DOMAIN
    -!- SIMILARITY: Contains 1 J domain.
                                                                                                                                                                                               EMBL; AF412025; AAM62307.1; --
EMBL; AK058113; BAB71671.1; --
EMBL; BC005056; AAH05056.1; --
Genew, HGNC16410; WBSCHB.
INTEXPRO; IPR001623; DnaJ.N.
INTEXPO; IPR001623; DnaJ.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bovine adrenal cortex.";
J. Biochem. 102:1333-1336(1987).
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J. Bacteriol. 184:5479-5490(2002).
-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
(SDR) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CDC 1551 / Oshkosh;
STRAIN=CDC 1551 / Oshkosh;
MEDLINE=2226494; PubMed=12218036;
MEDLINE=22266494; PubMed=12218036;
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Rolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman D., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=8029587; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eighmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd & Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitchead S., Barrell B.G., Encouplete genome sequence sequence sequence sequence sequence sequence my sequence in Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corymebacterinee; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                               57.0%; Score 49; DB 1; Length 492; llarity 83.3%; Pred. No. 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis
Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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NADPH:ADRENCDOXIN OXIDOREDUCTASE.
E -> EVLLCQ (in isoform Long).
/FITIGH-SVEP 0.003415.
G -> R (IN REF. 3).
FGVAPDHPEVKAVI -> VWLALTTPRSRMLL (IN REF.
                                                                                                                                                                                                                                                                                                                                                ODAYH -> RVYRLT (IN REF. 3).

K -> R (IN REF. 3).

S -> RL (IN REF. 3).

RAAGIRLAVTR -> ARRSAMOSPB (IN REF. 3).

TRAVPTGDVEDL -> HPGSAHWGCGGP (IN REF. 3).
                PIR; JT0751; JT0751.

PDB; ICCC; 12-APR-99.

PDB; IELL; 24-SEP-00.

PDB; IELL; 24-SEP-00.

PDB; IELN; 24-SEP-00.

PDB; IENN; ANXEDTANASE.

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   EMBL; X13736; CAA32002.1;
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204
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the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (Se http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Raft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.7%; Score 47; DB 1; Length 253; 100.0%; Pred. No. 10; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                        Tuberculist; Rv0945; -.
InterPro; IPR002199; ADH short.
Pfam; PF00106; adh short; 1.
PROSITE; PS00060; SDRFMILY.
PROSITE; PS00061; ADH SHORT; 1.
PROSITE; PS00061; ADH SHORT; 1.
PROSITE; PS00661; ADH SHORT; 1.
PS000FENCE 253 AA; 27138 MM; BAD937208842DA12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YD55_MYCTU STANDARD; PRT; 715 AA. 011025.
011025.
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2003 (Rel. 35, Last mnotation update)
10-0CT-2003 (Rel. 35, Last annotation update)
Hypochetical protein Rv1355c/MT1398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 184:5479-5490(2002).
                                                                                                                                                                                                                 EMBL; Z79700; CAB02005.1; -.
EMBL; AE006982; AAX45219.1; -.
PIR; G70715; G70715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 PWWPW 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                  TIGR; MT0971;
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YD55_MYCTU
AC 011025.
DT 01-0CT-
DD 10-0CT-
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           STANDAR AND STANDAR ST
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- MISCELLANEOUS: Component I catalyzes the formation of anthranilate
        using ammonia rather than glutamine, whereas component II provides
        glutamine amidotransferase activity.
        glutamine amidotransferase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    savastanoi.";
J. Bacteriol. 173:463-471(1991).
-!- CATALYTIC ACTIVITY: Chorismate + L-glutamine = anthranilate +
pyruvate + L-glutamate.
-!- PATHWAY: Tryptophan biosynthesis; first step.
-!- PATHWAY: Tetramer of two components I and two components II (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas syringae (pv. savastanoi).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=29418;
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MEDLINES-91100331, PubMed=1987141;
da Costa e Silva O., Kosuge T.;
"Molecular characterization and expression analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
54.7%; Score 47; DB 1; Length 715;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anthranilate synthase gene of Pseudomonas syringae subsp.
                                                                                                                                                                      EMBL, ABOOT012; ABAK5661.1; ALT_INIT.
PIR, B70741; B70741.
TIGR, MT1398; .
TUBACCULISH: RV1356; -.
INLETPRO; IPR009036; MoeB.
InterPro; IPR00594; Thir domain.
Pfam, PF00899; Thir; .
EMPOCHELICAL protein; Complete proteome.
SEQUENCE 715 AA; 78181 MW; 455495248A56041C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-FRZ-1991 (Rel. 14, Last annotation update)
Anthranilate synthase component I (EC 4.1.3.27).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   505 AA
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InterPro; IPR006805; Anth_synth_I.N.
InterPro; IPR005265; Anth_synthI.D.
Pfam; P004715; Anth synthI.D.
Pfam; PR00425; chorismate bind; 1.
PRINTS; PR00095; ANTSNTHAŠEI.
ProDom; PD000779; Anth_synth_chor; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M55911; AAA26016.1; -.
HSSP; Q06128; 1QDL.
                                                                                                                                  EMBL; Z75555; CAA99988.1; -. EMBL; AE007012; AAK45661.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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RWAYYPWRR 73
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P21689;
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Gaps

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DB 1; Length 196; 15; 2; Indels

52.3%; Scc. 50.0%; Pred. No. 15, 50.0%; Pred. No. 1

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Hypothetical protein.
SEQUENCE 196 AA; 22104 MW; 436764DA9E26074C CRC64;
                                                                                                              1 ILRWP-WW---PWRRK 12
                                                                                                                                         63 IYOWPGWWMGTPWKLK 78
                                            Query Match
Best Local Similarity 50.0
Matches 8; Conservative
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SEQUENCE
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WEDLINE=21848401; PubMed=11859360;

WeDLINE=21848401; PubMed=11859360;

WeDLINE=21848401; PubMed=11859360;

WeDLINE W., Gailliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Brooks K., Gonnor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gollins M., Connor R., Connor R., Markle E.J., Hunt S., Jagels K.,

James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

Molver K., O'Neil S., Mungall K., Marby L., Niblett D., Odell C.,

Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

Rodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Weltjens I., Vanstreels E., Rieger M., Schewer S.,

Rodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Rodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Rodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Rodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Rodel C., Fuchs M., Fritzc C., Helzer E., Moestl D., Hilbert H.,

Berrym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Purneller S.,

Golffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motier S.,

Lucas M., Rochet M., Gaillardin C., Tallada V.A., delzon A., Thode G.,

Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

Nature 415812-800(2002)

Nature 415812-800(2002)

Nature 415812-800(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: STRONG, TO BACTERIAL MODULATOR OF DRUG ACTIVITY B
                                                                                                13,
                                                               DB 1; Length 505;
                                                                                             3; Indels
                 Tryptophan biosynthesis; Tyase.
SEQUENCE 505 AA; 56084 MW; A38E81931331F6BB CRC64;
                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FBS-2003 (Rel. 41, Last annotation update)
Hypothetical protein C5H10.05c in chromosome I.
                                                              ; Score 45.5; DE; Pred. No. 31; 2; Mismatches
                                                                                                                                                                                                                                             196 AA
                                                                                                                                                           467 VLEWEETINKRRAMVGSAWWPWPR 491
                                                                                                                               1 ILRW------PWWPWRRK 12
 TIGRFAMS; TIGR00564; trpE_most; 1.
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InterPro, IPR003680, NADHdh 2.
Pfam, PF02525; Flavodoxin_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z49811; CAA89955.1; -. PIR; S55483; S55483.
                                                               52.9%;
                                            Query Match
Best Local Similarity 26.v.
7; Conservative
                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces.
NCBL_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                              RESULT 8
YA05_SCHPO
ID YA05_SCHPO
AC Q09677;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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RESULT 9

CN3B RAT

AC Q63085,

DT 15-UL-1998 (Rel. 36, Last sequence update)

DT 28-PEB-2003 (Rel. 41, Last annotation update)

DT 28-PEB-2003 (Rel. 41, Last annotation update)

DE CGMP-inhibited 3',5'-cyclic phosphodiesterase B (EC 3.1.4.17) (Cyclic DE GMP-inhibited phosphodiesterase B) (CGI-PDE B) (CGI-PDE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular cloning of the rat adipocyte hormone-sensitive cyclic GMP-inhibited cyclic nucleoside phosphodiesterase.";
J. Biol. Chem. 268:18573-18575(1993).
- I. FUNCTION: May play a role in fat metabolism.
- I. CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)0 =
                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleoside 5'-phosphate.
--- ENZYME REGULATION: Inhibited by cGMP.
--- SUSCELLULAR LOCATION: Membrane-bound (Potential).
--- TISSUE SPECIFICITY: Abundant in adipose tissues.
--- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Sprague-Dawley, TISSUB-Adipose tissue;
MEDLINE=93366761; PubMed=8395509;
Taira M., Hockman S.C., Calvo J.C., Taira M., Belfrage P.,
Manganiello V.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-PRO.
POLY-ALA.
POLY-ALA.
POLY-ASP.
POLY-GLU.
POLY-CLU.
MW, C9B5078C7D3ADD6D CRC64;
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Pred. No. 76;
0; Mismatches
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InterPro; IPR002073; PDEase.
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1108 AA; 123105 MW;
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SMART; SM00471; HDC.
1.
PROSTIE; PS00126; PDEASE I; 1.
Hydrolase; CGMP; Membrane.
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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FUT3 HUMAN STANDARD; PRT; 361 AA.
P21217; Q99448; Q99449;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Galactoside 3(4)-L-fucosyltransferase (EC 2.4.1.65) (Blood group Lewis alpha-4-fucosyltransferase) (Lewis FT) (Fucosyltransferase 3) (FUCT-SECUENCE FROM N.A.
MEDIATE=91032981; PubMed=1977660;
MEDIATE=91032981; PubMed=1977660;
"A cloned human cDNA determines expression of a mouse stage-specific embryonic antigen and the Lewis blood group alpha(1,3/1,4) fucosyltransferase.";
Genes Dev. 4:1288-1303(1990). "Alpha (1,3/1,4)fucosyltransferase (FucT-III) gene is inactivated by a single amino acid substitution in Lewis histo-blood type negative Cameron H.S., Szczepaniak D., Weston W., "Expression of human chromosome 19p alpha(1,3)-fucosyltransferase genes in normal tissues. Alternative splicing, polyadenylation, and Nishihara S., Yazawa S., Iwasaki H., Nakazato M., Kudo T., Ando T., Narimatsu H.; MEDLINE=94033579; PubMed=8219240; Kada Y., Kimura H., Mekada E.; "Analysis of Lewis fucosyltransferase genes from the human gastric mucosa of Lewis-positive and -negative individuals."; Blood 82:2915-2919(1993). VARIANTS LE(-) ARG-20 AND LYS-356.
MEDLINE=94342259; PubMed=8063716;
Mollicone R., Reguigne I., Kelly R.J., Fletcher A., Watt J.,
Chaffield S., Aziz A., Cameron H.S., Weston B.W., Lowe J.B., Oriol
"Molecular basis for Lewis alpha(1,3/1,4)-fucosyltransferase gene
deficiency (FUT3) found in Lewis-negative Indonesian pedigrees."; Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. VARIANT LE(-) MET-105.
MEDI-INE=94059067; PubMed=8240322;
Elmgren A., Kydberg L., Larson G.;
"Genotypic heterogeneity among Lewis negative individuals.";
Biochem. Biophys. Res. Commun. 196:515-520(1993). fucosyltransferase."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases TISSUE-Squamous cell carcinoma; Rahim I., Schmidt I.R., Wall D., Drayson E., Maslanik Stranahan P.L. Pettijohn D.E.; "Isolation and expression of human alpha (1,3/1,4) lochem. Biophys. Res. Commun. 196:624-631(1993). VARIANTS LE(-) ARG-20; SER-170 AND ALA-336. Biol. Chem. 270:20112-20122(1995) VARIANTS LE(-) ARG-20 AND SER-170. IISSUE=Liver; MEDLINE=95378269; PubMed=7650030; MEDLINE=94059082; PubMed=8240337 164 WQWWSWLR 171 III).
FUT3 OR LE OR FT3B.
Homo sapiens (Human). SEQUENCE FROM N.A. SEQUENCE FROM N.A. NCBI_TaxiD=9606 ndividuals. isoforms. RARRETTREEPRETTREEPRETTREEPRETTREEPRETTREEPRETTREEPRETTREEPRETTREEPRETTREEPRETTREEPRETTREEPRETTREEPRETTREEPRET 유

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REDLINE-9836698; PubMed-9703429;

REDLINE-POLY IN TRANSPORTED IN THE EXPRESSION OF VIM-2, LEWIS A. SIALYL

LEWIS AND LEWIS X/SSEA-1 ANTIGENS. MAY BE INVOLVED IN BLOOD GROUP LEWIS AND LEWIS NAY BE INVOLVED IN BLOOD GROUP LEWIS DETERMINATION; LEWIS-POSITIVE (LEC+)) INDIVIDUALS

RAVE AN INACTIVE BUZYME WHILE LEWIS-NEGATIVE (LEC+)) INDIVIDUALS

HAVE AN INACTIVE BUZYME WHILE LEWIS-NEGATIVE (LEC+)) INDIVIDUALS

HAVE AN INACTIVE BUZYME.

CHOOS OF THE STANSPERSON OF VIM-2, LEWIS A. LEWIS A. LEWIS A. LOSS A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE=97413801; PubMed=9268337; Elmgren A., Mollicone R., Costache M., Boerjeson C., Oriol R., Harrington J., Larson G.; "Significance of individual point mutations, T202C and C314T, in the human Lewis 'FUT3' gene for expression of Lewis antigens by the human alpha'1,3/1,4'-fucosyltransferase, Fuc-TIII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE=96243526; PubMed=8801770;
Elmgren A., Boerjeson C., Svensson L., Rydberg L., Larson G.;
"DNA sequencing and screening for point mutations in the human Lewis
'FUT3' gene enables molecular genotyping of the human Lewis blood
                                                                      VARIANT LE(-) LYS-356.
MEDLINE-95050753; PubMed=7961897;
Mishihara S., Narimatuh., Iwasaki H., Yazawa S., Akamatsu S.,
Ando T., Seno T., Mariumtsu I.;
"Molecular genetic analysis of the human Lewis histo-blood group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS LE(+) LYS-102 AND ALA-124, AND VARIANTS LE(-) ASN-162;
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EMBL, U27328; AAC50187.1; --
EMBL, U27327, AAC50186.1; --
EMBL, U27327, AAC50166.1; --
EMBL, D89324; BAA13941.1; --
EMBL, D89325; BAA13942.1; --
EMBL, AF131913; AAD33514.1; --
PIR, A3669; A3669.
MIM, 111100; --
GO, GO:0005624; C:membrane fraction; TAS.
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Biol. Chem. 269:20987-20994(1994).
                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 269:29271-29278(1994).
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Vox Sang. 70:97-103(1996)
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165
196
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165
196
162
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372 AA;
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Best Local Similarity
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ID ACT UT
AC Q1073;
C10773;
C10773;
C10-CCT-1996
DT 10-CCT-2003
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GN MYCODACTERIUR
CC COTYNEDACTERIUR
CN NCBI_TAXID=1
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SEQUENCE
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MEDLINE-98037800; PubMed=9368041;
Costache M., Apoil P.-A., Cailleau A., Elmgren A., Larson G.,
Costache M., Apoil P.-A., Coilleau A., Elmgren A., Larson G.,
Henry S., Blancher A., Iordachesou D., Oriol R., Mollicone R.;
"Evolution of fucosyltransferase genes in vertebrates.";
J. Biol. Chem. 272:29721-29728(1997).
-!-FUNCTION: May catalyze alpha-1,3 and alpha-1,4 glycosidic linkages involved in the expression of sialyl Lewis X and Lewis X/SSEA-1 antigens. It may be involved in blood group Lewis determination (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY_2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Galactoside 3(4)-L-fucosyltransferase (EC 2.4.1.65) (Blood group Lewis alpha-4-fucosyltransferase) (Lewis FT) (Fucosyltransferase 3) (FUCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1=VAR 003429.
K (IN LE(-); LESS THAN 10% REDUCTION
                                                                                                                                                                          SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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 S (IN LE(-); COMPLETELY INACTIVE).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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                                    InterPro; IPR00152. Tayloc trans 10.

Pfam; PF00852; Glyco transfera 10.

Transferae; Glycosyltransferaes; Glycoprotein; Transmembrane; Signal-anchor; Golgi stack; Polymorphism; Blood group antigen.

DOMAIN 1 15 CYTOPLASMIC (POTENTIAL).

TRANSMEM 16 34 SIGNAL-ANCHOR (TYPE-II MEMBRANR DI
                                                                                                                                                                                                                      LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (PROBABLE)
N-LINKED (GLCNAC. .) (PROBABLE)
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Pred. No. 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF4398044F19C284 CRC64;
GO; GO:0008417; F:fucosyltransferase activity; TAS. GO; GO:0005975; P:carbohydrate metabolism; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          S -> A (IN LE(+))

/ FTId=VAR 007961.

D -> N (IN LE(+))

/ FTId=VAR 00707.

G -> C
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/FTTd=VAR 003426.

W -> R (IN LE(-)).

/FTTd=VAR 007959.

Q -> K (IN LE(+)).

FTTd=VAR 007960.

I -> M (IN LE(-)).

/FTTd=VAR 003427.
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/FTIG=VAR 007964.

D -> A (IN LE(-)).

/FTIG=VAR_003429.
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(IN LE(-))
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/FTId=VAR
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Best Local Similarity 85.7%;
Matches 6; Conservative
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185
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019058;
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AC 019058P
DT 30-MAY.
DT 15-MAY.
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N-acetyl-D-glucosaminyl-R = GDP + beta-D-galactosyl-(1->1)-[alpha-L-fucosyl-(1->4)]-N-acetyl-beta-D-glucosaminyl-R.
-!-PATHWAY: Glycosylation.
-!-SUBCELULIAR LOCATION: Type II membrane protein. Membrane-bound form in trans cisterane of Golgi (By similarity).
-!-POLYMORPHISM: There are two alleles, A and B. Allele A has Arg-16 and Val-304. Allele B has Gly-162 and Met-304.
-!-MISCELLANEOUS: Also acts on the corresponding 1,4-galactosyl derivative, forming 1,3-L-fucosyl links.
-!-SIMILARITY: Belongs to the glycosyltransferase family 10.
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WEDLINE=9825987; PubMed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Cornor R.,

Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

Oliver S., Osborne J., Quall M., Rajandream M.A., Rogers J.,

Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

"Deciphering the biology of Mycobacterium tuberculosis from the

complete genome sequence.";

Mature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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165 N-LINKED (GLCNAC. .) (POTENTIAL)
196 N-LINKED (GLCNAC. .) (POTENTIAL)
162 R -> G (in allele B).
163 V -> M (in allele B).
163233 MW, 649CBF8BCA7BD74C CRC64;
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Pfam; PF00852; Glyco transf_10; 1.

Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal-anchor; Golgi stack; Polymorphism.

DOMAIN 1 14 CYTOPLASMIC (POTENTIAL).

TRANSMEM 15 34 SIGNAL-ANCHOR (TYPE-II MEMBRANE PI
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 1; Length 372;
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
MMPL6 OR THE Process mmpL6.
MMPL6 OR RVISS7 OR MT1608 OR MTCX48.08C.
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346 3
535 AA;
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053735;
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MML4_MYCTU
            SOUTH THE FEET AND A SOUTH THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation her Buropan Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as long as its in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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STRAIN=CDC 1551 / Oshkosh,
MEDINE=22206494, PubMed=12218036,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Earbert D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21848401; PubMed=11859360; MEDLINE-21848401; PubMed=11859360; Mood V., Gariliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgourco V., Gariliam R., Rajandream S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamin M., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K., James K., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
                                                                                                                                                                                                                                                                                                                   laboratory strains.";
J. Bacteriol. 184:5479-5490(2002).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the mmpL family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              678DC86E24472BF4 CRC64;
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Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
Schizosaccharomyces.
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15-UUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein C23C11.06c in chromosome I.
SPAC23C11.06C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, Z74020; CAA98334.1; -.
EMBL, AE007027; AAK45875.1; -.
PIR; B70763; AS70763.
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InterPro; IPR004869; MMPL.
Pfam; PF03176; MMPL; 1.
Hypothetical protein; Trans
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Matches 6; Conservative
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293
330
397 AA;
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013912;
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TRANSMEM
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YDW6 SCHPO
            HAPPEN SERVICE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
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Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor K., Malsh S.V., Warren T., Whitehead S., Taylor K., Taylor K., Amin Squares S., Stevens K., Amodawad J., Volckaert G., Aert R., Robben J., Grymonprez B., Moedian I., Vanstreels E., Rieger M., Schaefer M., Maller Amerijans I., Vanstreels E., Rieger M., Schaefer M., Mallert H., Berk M., Fritzc C., Holzer E., Moestl D., Hilbert H., Bger P., Zimmermann W., Wedler H., Reinhardt R., Pohl T.M., A Goffeau A., Cadieu E., Dreano S., Gloux S., Lelandt E., Mottier S., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Jumens J., Hunt C., Moore K., Hurst S.M., Lomes M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Shakovski G.V., Ussery D., Barrell B.G., Nurse P., Shakovski G.V., Ussery D., Barrell B.G., Nurse P., Hart Genome sequence of Schizosacharomyces pombe.";

"The genome sequence of Schizosacharomyces pombe.";

"The genome sequence of Schizosacharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=H37RV;
MEDLINE=98295987; PubMed=9634230;
MEDLINE=98295987; PubMed=9634230;
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Sulter S., Seeger K., Skellon S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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MyCobacterium tuberculosis.

Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales; Corymebacterinee; Mycobacterineae; Mycobacterineae; Mycobacterium.
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51.2%; Score 44; DB 1; Length 535;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60124 MW; A6AE149AAA2929E2 CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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TRANSMEM 55 75 POTENTI
TRANSMEM 82 102 POTENTI
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GeneDB SPombe; SPAC23C11.06c;
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MEDLINE=98295987; PubMed=9634230;
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                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                 MEDLINE-2006494, PubMed=12218036;
MEDLINE-22006494, PubMed=12218036;
MEDLINE-22006494, PubMed=12218036;
Pleistehmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Bishal W., Jacobs W.R. T., Weidman J., Khouri H., Gill J., Mikula A., Bishal W., Jacobs W.R. Tr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                     J. Bacteriol. 184:5479-5490(2002).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the mmpL family.
Deciphering the biology of Mycobacterium tuberculosis from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44; DB 1; Length 967; Pred. No. 89;
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                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome
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01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
MULAILVE membrane protein mmpL2.
MMPL2 OR RV0507 OR MT0528 OR MTCY20G9.34.
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TIGREAMS, TIGRO0833, actII; 1.
Hypothetical protein, Transmem
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           complete genome sequence.";
Nature 393:537-544(1998).
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InterPro; IPR004869; MMPL.
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                                                                                                                                                                                                                                                                                                                                     Tuberculist; Rv0450c;
                                                                                                                                            laboratory strains.";
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Matches 6; Conserv
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AC Q11171;
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             Harris D.
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S
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MEDLINE=2220644; PubMed=1218036;

Ple1schmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Ple1schmann R.D., Alland D., Eisen J.A., Earth D., Hickey E.,

Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,

Delcher A., Utterback T., Weinfann J., Khourt H., Gill J., Mikula A.,

Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;

"Whole-genome comparison of Mycobacterium tuberculosis clinical and
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Gole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Biglmeier K., Gas S., Barry C.E. III. Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamin N., Holroyd Hurneby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandram M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., Complete genome sequence.", Mycobacterium tuberculosis from the Nature 393:537-544 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Bacteriol. 184:5479-5490(2002).
-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-1- SIMILARITY: Belongs to the mmpL family.
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E -> A (IN REF. 2).
7; B68AE9B78164BDC0 CRC64;
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Pred. No. 90;
0; Mismatches
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PIR; F70746; F70746.
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Tuberculist; Rv0507; -.
Interpro; IPR04707; ActII.
Interpro; IPR004869; MMPL.
Pfam; PP03176; MMPL, 2.
TIGRFAM8; TIGR00833; actII; 1
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Best Local Similarity 75.0%;
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Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2004
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Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1017041 seqs, 315518202 residues Searched:

Total number of hits satisfying chosen parameters:

1017041

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

sp_fund::*
sp_human:*
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3: sp_fungi:* .01

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

	Description	Q8p4z9 xanthomonas	Q8ppu5 xanthomonas	Q9duc4 tt virus. o	Q84Bt7 oryza gativ	Q84zr3 oryza sativ	Q7u058 mycobacteri	Q9jh31 tt virus. o	Q84712 porcine epi	Q9lav1 porcine epi	Q8b482 porcine epi	Q8qq98 porcine epi	ш	Q8zu59 pyrobaculum	Q9y4n1 homo sapien	Q8djh5 synechococc	P96143 thermoactin
SUMMARIES	ΙD	5 Q8P4Z9	S QBPPUS	2 Q9DUC4	0 Q84ST7	0 Q84ZR3	6 Q70058	2 Q9JH31	2 Q84712	2 Q91AV1		2 080098	Q9Y7V5	7 Q8ZU59	Q9Y4N1	5 оврлн5	P96143
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æ	Query Match	68.6	68.6	66.3	62.2	62.2	61.6	61.6	61.6	61,6	61.6	61.6	60.5	59.3	59.3	59.3	59.3
	Score	93	59	57	53.5	53.5	53	53	23	53	53	53	52	51	51	51	51
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Q80VT9 Q9CZA1 Q8PG47 Q9AUN3 Q7XFD1	Q9DUC9 Q7V8S5 Q9DT80 Q19573 Q988W4	Q9DT81 Q91D04 Q8PE93 Q9X8C2	Q8LGM8 Q8ZNS5 Q8Z5Q0 Q8G7C2 Q84JN0 O07504	QBPHA9 QBV7E2 Q9SNN3 Q9HXC9 Q7ULX9 Q7UG74	11.
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## ALIGNMENTS

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SEQUENCE FROM N.A.

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RA MUSINIEZ-202145; PubMed-12024217;

RA Alves L.M.C., do Amaral A.M., Berrolnin M.C., Camargo L.B.A.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Berrolnin M.C., Camargo L.B.A.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Camarotte G., Cannavan F., Cardozo J., Lemos G.R., El-Dorry H.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Ferro M.I.T.,

RA Acsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.P.,

RA Acsuyama A.M., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins B.C., Machado M.A., Tamura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Trindade dos Santos M., Truffi D., Teai S.M., White F.F.,

RA Trindade dos Santos M., Truffi D., Teai S.M., White F.F.,

RA Trindade dos Santos M., Truffi D., Teai S.M., White F.F.,

RY "Comparison of the genomes of two Xanthomonas pathogens with differing

RY Mocuplete proteome.

RW Complete proteome.

SQUENCE 102 AA; 11488 MW, 641654465C9571BF CRC64; Xanthomonas campestris (pv. campestris). Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas. Last sequence update)
Last annotation update) Created) PRT; (TrEMBLrel. 22, C (TrEMBLrel. 22, L (TrEMBLrel. 22, L PRELIMINARY; Inner membrane protein NCBI_TaxID=340; 01-OCT-2002 ( 01-OCT-2002 ( 01-OCT-2002 ( Q8P4Z9 Q8P4Z9; XCC3549 RESULT 1 

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STRAIN=Mf-TTV9;
MEDLINE=20534983; PubMed=11080484;
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Query Match
Best Local Similarity 40.00,
Best Local 8, Conservative
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Matches 7; Conserv
                      [2]
SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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WEDLINE-2022145; PubMed-12024217;

da Silva AC.R., Ferro J.A., Reinach F.C., Furlan L.R.,
da Silva AC.R., Ferro J.A., Reinach F.C., Furlan L.R.,
da Guaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
A characotte G., Cannavan F.V., Cardozo J., Chambergo F., Ciaphia L.P.,
A Carelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
A crarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
A Formighieri B.P., Franco M.C., Greggio C.C., Gruber A.,
A Formighieri B.P., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,
A Formighieri B.C., Machado M.A., Madeira A.M.B.N., Martinez Rossi N.M.,
A Locali B.C., Machado M.A., Madeira A.M.B.N., Martinez Rossi N.M.,
A Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Cliveira V.R.,
A Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
A Spinola L.A.R.F. Tarkita M.A., Tamira R.B., Teixeira B.C., Tezza R.I.D.,
RA Stubal J.C., Kitajima J.P.,
T. "Comparison of the genomes of two Xanthomonas pathogens with differing
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadacee; Xanthomonas.
NCBI_TaxID=92829;
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         Score 59; DB 16; Length 102;
Pred. No. 1.2;
0; Mismatches 1; Indels
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Best Local Similarity 87.5%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 1; Indels
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
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Last annotation update)
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NCBI_TaxID=68897;
                                                                                                                                                                                                                                                                                                                                                         105 AA.
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EMBL: AE011686; AAM35479.1; -.
      Similarity 87.5%; 7; Conservative (
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(TrEMBLrel. 16, I
(TrEMBLrel. 25, I
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                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                         64 LRWPWWAW 71
                                                                                                                               2 LRWPWWPW 9
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Query Match
Best Local Similarity
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01-MAR-2001 (
01-OCT-2003 (
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Q8PPUS;
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                                                                    Matches
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Okamoto H., Nishizawa T., Tawara A., Peng Y., Takahashi M.,
Kishimoto J., Tanaka T., Miyakawa Y., Mayumi M.,
"Species specific TT viruses in humans and nonhuman primates and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Overton II.L., Tsitrin T., Xim M., Bera J.J., Jin S.S.,
Fadrosh D.W., Tallon L.J., Koo H., Zismann V. Hsiao J., Blunt S.,
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
White O., Salzberg S.L., Fraser C.M.,
"Oryza sativa chromosome 3 BAC OSJNBa0022N01 genomic sequence.",
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein CSJNB0092N01.27.
0SJNBA0092N01.27.
0SJNBA0092N01.27.
SLARATYOLA; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryzea.
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Pred. No. 7.4;
1; Mismatches 2; Indels 9;
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; AC120535, AAO73229.1;
Hypothetical protein.
SEQUENCE 137 AA, 15795 MM; 67E62CFAD153CB99 CRC64;
                                                                                           phylogenetic relatedness.";

Virology 277:368-378(2000).

EMBL, AB041959; BAB19313.1;

GO: GO:0004185; Freezine carboxypeptidase activity; IEAGO: GO:0004185; Freezine carboxypeptidase activity; IEAGO: GO:0004285; Freezine carboxypeptidase activity; IEAGO: GO:0004285; Freezine carboxypeptidase activity; IEAGO: GO:0004285; Freezine carboxypeptidase sio.

InterPro; IRR001563; Peptidase Sio.

InterPro; IRR001563; Peptidase Sio.

InterPro; IRR001563; Peptidase Sio.

Prosine: PROSISE; FREEZINET SER SER; I.

PROSITE; PS00131; CARBOXYPEPT SER SER; I.

SEQUENCE 723 AA; 85393 MW; 232D003098766344 CRC64;
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Q842R3
ID Q84Z1
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"Sequence analysis of the porcine epidemic diarrhea virus genome between the nucleocapsid and spike protein genes reveals a polymo."; Virology 198:466-476(1994).
EMBL: Z25483; CAA80971.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spike protein.
Porcine epidemic diarrhea virus (strain Br1/87) (PEDV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duarte M., Laude H.;
"Sequence of the spike protein of the porcine epidemic diarrhoea
                                                                                                                                                                                                                                 Ukita M., Okamoto H., Nishizawa T., Tawara A., Takahashi M.,
Ilzuka H., Miyakawa Y., Mayumi M.,
"The entire mucleotide sequences of two distinct TT virus (TTV)
isolates (TJN01 and TJN02) remotely related to the original TTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIJNE=93389431; PubMed=8397280; MEDIJNE=93389431; PubMed=8397280; Bridgen A., Daarte M., Tobler K., Laude H., Ackermann M.; Eliden A., Duarte M., Tobler K., Laude H., Ackermann M.; Sequence determination of the nucleocapsid protein gene of the porcine epidemic diarrhoea virus confirms that this virus is a coronavirus related to human coronavirus 229E and porcine transmissible gastroenteritis virus.";
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MEDLINE-94120721; PubMed-8291230;
Duarte M., Tobler K., Bridgen A., Rasschaert D., Ackermann M.,
Laude H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 53; DB 12; Length 746; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                         Okamoto H.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                               88561 MW; E0B22953AE764E3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                Viruses; ssDNA viruses; Circoviridae; Anellovirus.
NCBI_TaxID=68887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1383 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                STRAIN=TJN02;
MEDLINE=20456801; PubMed=11003468;
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=94231173; PubMed=8176382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Gen. Virol. 75:1195-1200(1994)
[2]
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InterPro; IPR002552; Corona_S2.
Pfam; PF01600; Corona_S1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    61.6%;
54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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Best Local Similarity
Matches 6; Conserv
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                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                        STRAIN=TUN02;
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                 rr virus.
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STROIBNUE ruc.
STROIBNUE PAPE1122/97;
MEDLINE-22709107; PubMed=12788972;
MEDLINE-22709107; PubMed=12788972;
Garnier I., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Garnier I., Eiglmeier K., Carodin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Moseler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.,
"The complete genome sequence of Mycobacterium bovis.",
"The complete genome sequence of Mycobacterium bovis.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                  Oryza Bativa (japonica cultivar-group).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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Sasaki T., Matsumoto T., Yamamoto K.;
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC clone:OJ1372_D12.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP003827; BAC57651.1;
SEQUENCE 225 AA; 23825 MW; 52096C5EA0083F77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1765;
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         (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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01-JUN-2003 (TrEMBLE)
0J1372 D12.7 protein.
0J1372 D12.7.
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MEDLINE=S8455678; PubMed=9782358;
Bridgen A., Kocherhans R., Tobler K., Carvajal A., Ackermann M.;
Bridgen A., Kocherhans R., Tobler E., Carvajal A., Ackermann M.;
Further analysis of the genome of por
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                           Porcine epidemic diarrhea virus (strain CV777) (PEDV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93389433; PubMed=8397280; Bridgen A., Darte M., Tobler K., Laude H., Ackermann M.; Bridgen A., Duarte M., Tobler K., Laude H., Ackermann M.; Sequence determination of the nucleocapsid protein gene of the porcline epidemic diarrhea virus confirms that this virus is a coronavirus related to human coronavirus 229E and porcine transmissible gastroenteritis virus.";
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Duarte M., Tobler K., Bridgen A., Rasschaert D., Ackermann M.,
                                                                       61.6%; Score 53; DB 12; Length 1383; 62.5%; Pred. No. 67; arive 2; Mismatches 1; Indels (
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Kocherhans R., Bridgen A., Ackermann M., Tobler K.;

"The complete genome sequence of porcine epidemic diarrhea
Pfam; PF01601; Corona S2; 1. CONFLICT 422 42\frac{2}{2} Y -> N (IN REF. 1). SEQUENCE 1383 AA; 151405 MW; 741C84D5DD3BDC4D CRC64;
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InterPro; IPR002551; Corona_S1.
InterPro; IPR002552; Corona_S2.
Pfam; PF01600; Corona_S1.
Pfam; PF01601; Corona_S2; 1.
SEQUENCE_1383 AA; 151352 MW; 022E5E5E5435876D CRC64;
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                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                       PRT; 1383 AA.
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MEDLINE=96112302; PubMed=8830538;
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                                                     Query Match
Best Local Similarity 62.50
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EMBL; AF500215; AAM19716.1; -.
InterPro; IFR00255; Corona S1.
InterPro; IFR00255; Corona S2.
Pfam; PF01600; Corona S2:
InterPro Corona S2:
Embl. FF01601; Corona S2:
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STRAIN-chinju99;

Fee S.-G., Krell P., Nagy E.;

"Cloning and nucleotide sequence analysis of spike gene of porcine epidemic diarrhea virus detected in Korea.";

Submitteed (OCT-2002) to the EMBL/GenBank/DDBJ databases.

ENBL; AY167585; AAN86621.1; -.

InterPro; IPR002551; Corona.51.

InterPro; IPR002552; Corona.52.

Pfam; PF01600; Corona.81; 1.

Pfam; PF01601; Corona.81; 1.

Pfam; PF01601; Corona.81; 1.

SEQUENCE 1383 AA; 151582 MW; BSBA4D7EE5371A54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses, ssRNA positive-strand viruses, no DNA stage, Nidovirales, Coronaviridae, Coronavirus.
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Viruses; BRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Cronavirus.
NCBI_TaxID=28295;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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R Fungal Genet. Biol. 7:88-99 (1999).

R FASSP, PO1180; INCA.

GO, GO: 0005923; C:tight junction; IEA.

GO; GO: 000593; C:tight junction; IEA.

R GO; GO: 0005983; C:tight junction; IEA.

R GO; GO: 0005983; C:tight junction; IEA.

R InterPro; IPR001673; S mold repeat.

R InterPro; IPR001673; S mold repeat.

R PROSITE; PS01146; C:Laulin repeat.
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Proc. Natu. ",
Proc. Natu. ",
BMBL, AE009902, AAL64549.1; -.
GO; GO:0004156; F:dihydropteroate synthase activity; IEA.
GO; GO:0003396; P:folic acid and derivative biosynthesis; IEA.
InterPro; IPR000489; DHPS.
InterPro; IPR006399; DHPS.
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STRAIN=IM2 / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                               Trichoderma harzianum.
Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Hypocreomycetidae; Hypocreales; Hypocrea.
NCBI_raxID=5544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.5%; Score 52; DB 3; Length 1245; 60.0%; Pred. No. 82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 AA; 32885 MW; 0A463F36739D3ED1 CRC64;
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                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
                                         PRT; 1245 AA
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TIGRPAMS; TIGR01496; DHPS; 1.
Complete proteome.
SEQUENCE 298 AA; 32885 MW;
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Archaea; Crenarchaeota; Thermc
Thermoproteaceae; Pyrobaculum.
NCBI_TAXID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8ZU59;
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 60.0-
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                                      PRELIMINARY;
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SEQUENCE FROM N.A.
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Q9Y7V5
ID Q9Y7V5
                                                                     Q9Y7V5
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Q8ZU59
                                         PACOCCOS ON THE SECTION OF THE SECTI
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MEDLINE-2225144; PubMed=12240834;
MEDLINE-2225144; PubMed=12240834;
A Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., A Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kimoko A., Katanabe A., Iriguchi M., Rawashima K., Makazaki N., A Shimpo S., Sugimoto M., Takeunoto M., Matanah M., Tabata S.;
"Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
DNA Res. 9:123-130(2002)
R EMBL; AP005373; BAC08802.1; -.
R InterPro; IPR01678; Sun. Nopl/Nop2.
R Ffam; Pf01189; No11_Nop2_Sun; 1.
R Ffam; Pf01189; No11_Nop2_Sun; 1.
SEQUENCE 351 AA; 38494 MW; 675046ADCBE7C835 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUB-Testis;
Ansorge W., Wirkner U., Mewes H.W., Gassenhuber J., Wiemann S.;
Submitted (JVN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL096753; CAB46428.2; -.
PIR; T12505; T12505.
Hypothetical protein.
NON TER
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0
59.3%; Score 51; DB 17; Length 298;
ilarity 71.4%; Pred. No. 31;
Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 299 AA; 34032 MW; 6B8DB60E6A88239A CRC64;
                                                                                                                                                                                                                                                                                                          Q9Y4N1 PRELIMINARY; PRT; 299 AA. 09Y4N1, CTEMBLED. 12, Created) 01-NOV-1999 (TrEMBLED. 13, Last sequence update) 01-MAY-2000 (TrEMBLED. 13, Last sequence update) Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                  :|||| |
209 QWPWWKW 215
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Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                 3 RWPWWPW
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TLR1250.
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Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Search completed: May 4, 2004, 15:22:10 Job time: 32.2281 secs

protein search, using sw model OM protein -

May Run on:

4, 2004, 15:08:11 ; Search time 49.6053 Seconds (without alignments) 74.047 Million cell updates/sec

US-09-444-281-85 99

1 ILPWKWPWWRR 13 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 Total number of hits satisfying chosen parameters:

1586107 segs, 282547505 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* A_Geneseq_29Jan04:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp20048:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	-	7 Indoli	Aaw66441 Cationic	Aay24608 Indolicid	6	Aay44666 Crosslink	4	0	1 Amino	2 Amino a	3 Natura		4		Abp60382 Indolicid		Bovine c	4	Abp59052 Peptide #	111	Abb81249 Indolicid	Abb81261 Indolicid		Ada00505 Antimicro	Ada00504 Antimicro
SUMMARIES		QI	AAR30970	AAR78457	AAW66441	AAY24608	AAW87609	<b>AAY44666</b>	AAY44324	AAY91740	AAY91771	AAY91772	AAY57123	AAY55056	AAY92794	AAB91842	ABP60382	ABP60383	ABB07699	ABB81940	ABP59052	AAU90977	ABB81249	ABB81261	AA015561	ADA00505	ADA00504
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ABU59617 ABG76068 AAE34433	ABR00800 ABR00815 ABR63788				AAY44668 AAY57142 ABB07706 AAR78459
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# ALIGNMENTS

AAR30970 standard; peptide; 13 AA. (first entry) (revised) 25-MAR-2003 12-MAY-1993 AAR30970; RESULT 1 AAR30970 

Broad spectrum antimicrobial indolicidin peptide

Tryptophan rich; microbial; microbistatic; inhibition.

Bos taurus.

WO9222308-A1

23-DEC-1992

92WO-US004920. 10-JUN-1992;

91US-00715271. 14-JUN-1991;

(REGC ) UNIV CALIFORNIA.

Cullor JS; Selsted ME,

WPI; 1993-017896/02.

Broad spectrum antimicrobial cpd. obtd. from bovine granulocytes -comprises tryptophan rich peptide, pref. having low immunogenicity and comprising proline rich peptide or carboxy terminal amide.

Claim 2; Page 19; 29pp; English.

The sequence is that of an indolicidin peptide which shows broad spectrum antimicrobial activity and when administered to a host does not elicit an immune response. It is effective against virtuses, gram positive bacteria, gram negative bacteria and fungi, including Staphylococcus aureus. Escherichia coli, Salmonella typhimurium, Listeria monocytogenes, Candida albicans and Cryptococcus neoformans. It can be used as a therapeutic agent, food preservative or disinfectant, e.g. to purify a water supply. The peptide is pref. administered at an effective amt. of 0.5-500 ug/ml final concentration. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 13 AA;

Query Match

DB 2; Length 13; 100.0%; Score 99;

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AAW66393 to AAW66469 represent native cationic peptides from the present treating infection, especially bacterial infections. The compositions and methods for methods use cationic peptides in combination with an antibiotic agent which are then administered to a patient to enhance the activity of the antibiotic agent, to overcome: (a) tolerance; (b) acquired resistance; and (c) inherent resistance. The combinations of antibiotics and cationic peptides can provide synergistic activity against a microorganism that is tolerant, inherently resistant, or has acquired resistance to an antibiotic agent. They can be used for killing e.g. bacteria, fungi, parasites and viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indolicidin, bacterial infection, photo-oxidised solubiliser, additive, antimicrobial, antibiotic, antiarrythmic, surface disinfectant, additive,
                                                                                                                                                                                           Indolicidin analogue, resistance, cationic peptide, antibiotic, oacteria, infection, tolerance, antibacterial, microorganism, bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New indolicidin peptide analogues - useful for, e.g. enhancing activity of antibiotic or overcoming tolerance, acquired resistance or inherent resistance of microorganisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 99; DB 2; L. 100.0%; Pred. No. 1.4e-06; iive 0; Mismatches 0;
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                         AAW66441 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mcnicol PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY24608 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MICR-) MICROLOGIX BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0040649P.
97US-00915314.
97US-0060099P.
98US-00030619.
                                                                                                                                                  Cationic peptide indolicidin.
                                                                                                                                                                                                                                                                                                                                                                                                               98WO-CA000190.
                                                                                                             (first entry)
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nes 13; Conservative
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                                                                                                                                                                                                                                      fungus; parasite; virus.
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20-AUG-1997;
26-SEP-1997;
25-FEB-1998;
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                                                                                                             12-JAN-1999
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                                                                                                                                                                                                                                                                                 Bos taurus.
                                                                  AAW66441;
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Matches
    AAY24608
ID AAX2
XX
AC AAY2
XX
DT 18-P
XX
DE Indc
XX
KW Indc
KW anti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequences represented by AAR78454-R78459 are indolicidin analogues.
These analogues exhibit broad spectrum antimicrobial activity and have analogues exhibit broad spectrum antimicrobial activity of antimicrobial selectivity when compared to naturally occuring indolicidin. The antimicrobial activity of these analogues can be altered by incorporation of D-form, chemically altered or synthetic amino acids.
These sequences can be incorporated into a pharmaceutical composition (e.g. as a liposome or non-liposome lipid complex carrier) for use in a microbicidal method. These sequences are active against Gram positive and negative bacteria, protozoa, yeast, fungi and viruses. They can be used as therapeutic agents, prophylactics, food preservatives, disinfectants or medications. These sequences are easily synthesised in an active and effective broad spectrum antimicrobial form with decreased undesirable side effects. Compared to naturally occuring indolicidin, these analogues cannow increased antimicrobial and decreased haemolytic activity. Peptide stability, and period of activity within the cell can be increased or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Analogues of the tryptophan-rich peptide indolicidin - exhibiting broad spectrum antimicrobial activity and selectivity without undesirable side
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Indolicidin, microbicide, therapeutic agent; prophylactic;
food preservative, disinfectant; medication; Gram positive bacteria;
Gram negative bacteria; protozoa; yeast; fungi; viruses.
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  Pred. No. 1.4e-06;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Match
Local Similarity 100.0%; Pred. No. 1.4e-06; Pred. 13; Conservative 0; Mismatches 0:
                                                                                                                                                                                                               AAR78457 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 27; 37pp; English.
Best Local Similarity 100.0%; P Matches 13; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-00197205
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                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                           ILPWKWPWWPWRR 13
                                                               1 ILPWKWPWWRR 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA,
                                                                                                                                                                                                                                                                                                                                             Indolicidin analog #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-302552/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9522338-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-FEB-1994;
                                                                                                                                                                                                                                                                                                    25-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-AUG-1995
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Synthetic

RESULT 2 AAR78457

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Gaps

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Query Match

Best Loca Matches

RESULT 3

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Length 13; Indels peptide

Ï Lee

Kim JH, Hong S,

Lee JH, Kang MH,

KOREA ADV INST SCI & TECHNOLOGY.

SAMYANG GENEX CORP

98WO-KR000132

98KR-00013372

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New method for mass production of antimicrobial peptides - by constructing fusion genes comprising acidic and antimicrobial genes and transforming host with vector containing these.
                                                                                                                                                                                                                                                                                                                         Example 6; Page 18; 52pp; English
                                                                                                                                                                                                                               WPI; 1999-059844/05.
                                                                                                                                                                                                                                            N-PSDB; AAV83788
                                             WO9854336-A1.
                                                                                               28-MAY-1998;
                                                                                                                         28-MAY-1997;
                                                                                                                                     09-APR-1998;
                                                                    03-DEC-1998
                                                                                                                                                               (SAMY-)
                                                                                                                                                                             (KOAD)
                     Bos ap.
                                                                                                                                                                                                      Kim S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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ID AAY4
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                                                                                                                                                                                                                                                                                                                                                       AAY24549 to AAY24615 represent indolicidin analogues of formulae (I)-
(VIII) containing up to 25 amino acids (aa): RXZXXZXB (I), BXZXXZXB (II),
BBBAXZXXZXB (II), BXZXXZXBBBI (AA), MMILBBAGS (IV), BXZXXZXBBA, AM (V),
LBBAXZAXZXRK (VI), LKAXZXXXBBBI (AA), MHORE Z
COF K; AA = any aa; n = 0 or 1; in (II), at least I Z = V; in (VIII) at
least 2 X = F or Y . The analogues are used to treat infections caused by
bacteria (Gram positive or negative, or anaerobic); fungi (yeast or
moulds); parasites (protozoa, nematodes, cestodes or trematodes) or
viruses. Typical of very many pathogens that can be controlled are
Leishmania, Trypanosoma, Ascaris lumbricoides, Fasciola hepatica,
clostridium, rotavirus and papilloma virus. Compounds derived
from the analogues may be used smilarly; the compounds may also be
from the analogues may be used smilarly; the compounds may also be
used therapeutically or to coat medical devices; also they are useful as
surface disinfectants, as additives to shampoo or soaps, as insecticides
or herbicides, or as preservatives for foods and technical materials.
Corberbally at 0.1-50 mg/kg. These analogues have a broader spectrum of
activity than indolicidin and modification as compounds reduces their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                 New indolicidin analogues with antimicrobial activity and related nucleic acid - vectors, transformed cells and antibodies, also conjugates with polyoxyalkylene glycol and fatty acid to reduce toxicity, useful therapeutically, as disinfectants etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antimicrobial; fusion; acidic peptide; recombinant; microorganism; guamerin; basic peptide; Indolicidin.
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shampoo; soap; insecticide; herbicide; preservative; food;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 99; DB 2; Length 13;
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                                                                                                                                                                                                                Taylor R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                     Example 1; Page 32; 129pp; English
                                                                                                                                                                                                             Fraser JR, West MH, Krieger TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW87609 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antimicrobial peptide Indolicidin.
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                                                                                                                                                                                    (MICR-) MICROLOGIX BIOTECH INC.
                                                                                                                                            96US-0024754P.
97US-0034949P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILPWKWPWWPWRR
                                                                                                                                                                                                                                         WPI; 1998-169090/15.
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Best Local Similarity
              technical material
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13 AA;
                                                                                                                   21-AUG-1997;
                                                                  WO9807745-A2
                                                                                                                                            21-AUG-1996;
13-JAN-1997;
                                                                                           26-FEB-1998
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                                       Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             toxicity
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The invention relates to mass production of antimicrobial peptides. The method comprises constructing a fusion gene containing a first gene encoding a negatively charged acidic peptide having at least two cysteine residues, and a second gene encoding a peptide having at least two cysteine antimicrobial peptide. A host microorganism is transformed with a vector containing the fusion gene and then cultured. The expressed antimicrobial peptides in recombinant microorganisms. The inhibitory effect of the expressed antimicrobial peptides in recombinant microorganisms. The inhibitory effect of the expressed antimicrobial peptide upon the growth of the host microorganism is considerably reduced by fusing it to the acidic peptide. Therefore, the use of the fusion gene provides an economic, recombinant alternative of mass producing antimicrobial peptides, which overcomes the disadvantages of low-productivity and poor economy, previously encountered by recombinant and chemical methods. The present sequence represents an antimicrobial peptide Indolicidin. The encoding DNA can be used and and acidic peptide Guamerin gene in the construction of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Crosslinked indolicidin analog; X-indolicidin; Indol 1-13(W6/9); stability; bovine neutrophil; antimicrobial; antibacterial; fungicide; protozoacide; virucide; anti-HIV; human immunodeficiency virue-1; HIV-1; gram positive bacteria; gram negative; Staphylococcus aureus; HIV-1; Escherichia coli; Salmonella typhimurium; yeast; fungi; protozoa; Candida albicans; Cryptococcus neoformans; Giardia; Acanthamoeba.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch
1 Similarity 100.0%; Pred. No. 1.4e-06;
13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY44666 standard; peptide; 13 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the fusion gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13 AA;
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The present amino acid sequence is an antimicrobial peptide, Indolicidin derived from cow, Bos taurus. It is used along with a derivative of purF gene sequence that functions as a fusion partner. A DNA construct that comprises, this antimicrobial peptide encoding sequence and the entire, partial or derivative of purF gene, is used for mass production of the antimicrobial peptide in microorganisms without killing the host cells. Use of the purF gene derivative sequence, neutralises the toxicity of the antimicrobial peptides against the host microorganism. The antimicrobial peptides are useful commercially in the pharmaceutical and food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cationic peptide; tumour; pharmaceutical composition; cancer; treatment; leukaemia; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma; breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon;
                                                                                                                                                                                                                                 w DNA constructs useful for mass production of antimicrobial peptides microorganism hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel pharmaceutical composition containing optionally activated polyoxyalkylene-modified cationic peptides, useful for treating tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
                                                                                                                                                  Lee H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                  Hong SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 99; DB 3; D
100.0%; Pred. No. 1.4e-06;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cationic peptide Indolicidin amino acid sequence.
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                                                                                                                                                  Lee JW,
                                                                                                                                                  Park SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY91740 standard; peptide; 13 AA.
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                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1; 67pp; English.
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                  99WO-KR000282.
                                                    98KR-00022117
                                                                                                             (SAMY-) SAMYANG GENEX CORP.
                                                                                                                                                    Kang MH, Lee J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUN-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      multidrug resistance
                                                                                                                                                                                     WFI; 2000-097542/08.
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                         N-PSDB; AAZ44324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13 AA;
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                                                    09-JUN-1998;
14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    industries
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                                                                                                                                                    Kim JH,
                                                                                                                                                                                                                                              New DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The patent discloses crosslinked analogs of indolicidin (Indol 1-13) which is a naturally occurring peptide isolated from bovine neutrophils and has antimicrobial activity. The crosslinked indolicidin (X.-indolicidin) analogs are stable and have antimicrobial activity against gram positive and negative bacteria (e.g. Staphylococcus aureus, Escherichia coli and Salmonalla typhimurium), yeasts and fungi (e.g. Candida albicans, Cryptococcus neoformans), protococa (e.g. Giardia species and Acanthamoeba species), and viruees (e.g. Giardia in an environment e.g. a food or food produt, a solution, an inanimate object comprising a surface, or a mammal. The present sequence is a specifically claimed X-indolicidin analog, indol 1-13(66/9) which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               purF gene; glutamine pyrophosphoribosyl pyrophosphate amidotransferase; purF derivative; fusion partner; antimicrobial peptide; Indolicidin; pars production; cleavage site; hydroxylamine; CNBr; DNA construct; cow; neutralise; toxicity; pharmaceutical industry; food industry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       Crosslinked indolicidin analogs with antimicrobial activity against
bacteria, yeast, fungi, protozoa and viruses.
                                                                           di-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
                                                               /note= "Residues at positions 6 and 9 form a tryptophan crosslink"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                /note= "C-terminal amide"
                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antimicrobial peptide, Indolicidin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 39; 53pp; English.
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                                                                                                                                                                                                                                                                                    98US-00099631.
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                Osapay K;
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-147133/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13 AA;
                                                    Modified-site
                                                                                                           Modified-site
                                                                                                                                                                    WO9965510-A1
                                                                                                                                                                                                                                                                                    18-JUN-1998;
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AAY44324;

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                                  This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxyalkylene (APO) -modified cationic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with a multiding resistant phenotype. The pharmaceutical composition can be used to treat tumours, specifically lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary, cervix, uterus, skin, prostate, liver and colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxyalkylene (APO) modified cationic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with a multidrug resistant phenotype. The pharmaceutical composition can be used to treat tumours, specifically lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary, cervix, uterus, skin, prostate, liver and colon
                                                                                                                                                                                                                                                                                                                                                                                                                               Cationic peptide; tumour; pharmaceutical composition; cancer; treatment; leukaemia; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma; breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon; multidrug resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                West MHP;
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel pharmaceutical composition containing optionally activated polyoxyalkylene-modified cationic peptides, useful for treating (
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fraser JR,
                                                                                                                                                                                         Length 13;
                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                     Score 99; DB 3; I. Pred. No. 1.4e-06; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Erfle D,
                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of cationic peptide MBI 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Krieger TJ, Taylor R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 14; 94pp; English.
            Disclosure; Page 11; 94pp; English.
                                                                                                                                                                                                                                                                                                                               AA.
                                                                                                                                                                                                                                                                                                                             AAY91771 standard; peptide; 13
                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MICR-) MICROLOGIX BIOTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-00096541.
                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                         1 ILPWKWPWWPWRR 13
                                                                                                                                                                                                                                                               ILPWKWPWWPWRR 13
                                                                                                                                                                                                 Local Similarity 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-223549/19.
                                                                                                                                                              Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Friedland HD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9965506-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                       AAY91771;
                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                       RESULT 9
                                                                                                                                                                                                                                                                                                                    AAY91771
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Length 13;

DB 3.;

100.0%; Score 99;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxyalkylene (APO)-modified cationic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with a multidary resistant phenotype. The pharmaceutical composition can be used to treat tumours, specifically lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary, cervix, uterus, skin, prostate, liver and colon
                                                                                                                                                                                                                                                                                                                                                                                                               Cationic peptide, tumour; pharmaceutical composition; cancer; treatment; leukaemia; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma; breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel pharmaceutical composition containing optionally activated polyoxyalkylene-modified cationic peptides, useful for treating tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               West MHP
                      Gaps
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                      Indels
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Pred. No. 1.4e-06;
0; Mismatches 0;
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ilarity 100.0%; Pred. No. 1.4e-06;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of cationic peptide MBI 10CN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ď,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Taylor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 14; 94pp; English.
                                                                                                                                                                                                                                 AAY91772 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY57123 standard; peptide; 13 AA.
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                                                                                                                                                                                                                                                                                                                           06-JJN-2000 (first entry)
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                                                                    1 ILPWKWPWWPWRR 13
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                          Conservative
                                                                                                                ILPWKWPWWPWRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           multidrug resistance
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Friedland HD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9965506-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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                                                                                                                                                                                       RESULT 10
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                                                                                                                                                                                                                AAY91772
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Indolicidin; bactenecin; sulphate-reducing bacteria; growth inhibitor; corrosion; degradation; metal; concrete, cement; dental implant; biofilm.

Non-amidated indolicidin peptide.

(first entry)

23-FEB-2000

AAY55056;

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indolicidin analogs, active against bacteria, yeast, fungi, protozoa virus, used for, e.g. treating infections.
                     Indolicidin analogue, antimicrobial activity, helminth, bacteria, virus, treatment, inhibit growth, micro-organism, contact lens solution, transgenic plant, surgical instrument, yeast, fungi, protozoa.
Naturally occurring bovine indolicidin peptide Indol 1-13.
                                                                                                                         /note= "C-terminal amide"
                                                                                          Location/Qualifiers
13
                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 28; 62pp; English
                                                                                                                                                                                                                            98US-00076227
                                                                                                                                                                                                    99WO-US009942
                                                                                                                                                                                                                                                   (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cells of such organisms
                                                                                                                                                                                                                                                                                                       WPI; 2000-053028/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13 AA;
                                                                                                            Modified-site
                                                                                                                                                   W09958141-A1
                                                                                                                                                                                                    05-MAY-1999;
                                                                                                                                                                                                                            12-MAY-1998;
                                                                                                                                                                           18-NOV-1999
                                                                                                                                                                                                                                                                                Selsted ME;
                                                                          Bos sp
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Inhibiting growth of sulfate-reducing bacteria using other bacteria, particularly for protection of metals and concrete.

Example 4; Page 41; 84pp; English

Barthman JC;

Jayaraman A,

Wood TK,

WPI; 2000-052882/04

(REGC ) UNIV CALIFORNIA

99WO-US009675, 98US-00074037.

03-MAY-1999; 06-MAY-1998; 31-MAR-1999;

WO9956553-A1 Bacillus sp.

11-NOV-11999.

This sequence represents the non-amidated indolicidin peptide. The invention relates to a method for inhibiting growth of sulphate-reducing bacteria (A) on a macerial (B) sensitive to corrosion or degradation, by applying to (B) a bacterium (C) that secretes a compound (I) able to inhibit growth of (A). The method is used to protect metal, concrete or cement against corrosion and degradation, but (B) can also be used to protect dental implants. (B) is present in an open or closed system (e.g. water cooling tower, liquid storage container, fuel tank, sewer or drainage system etc.) or part of a bridge or other structure. The method is more effective and less expensive than known methods for inhibiting (A), and reduces the amount of toxic chemicals released. Conventional biofilms of aerobic organisms tend to encourage growth of (A), and addition of (C) to the biofilm prevente this. A single application of (C) lasts for a long time, and (I) are produced exactly where they are required and inhibit (A) without significant impact on other organisms the biocides, which may then be used in reduced amounts). If local damage to the biofilm occurs, the underlying material is still protected by diffusion of (I) from neighbouring areas

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Magainin; antimicrobial; transgenic plant; protease degradation; Rev4;
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0
                                                                                                                                                                                                                                               Length 13;
                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                               Score 99; DB 3; I
Pred. No. 1.4e-06;
                                                                                                                                                                                                                                                                                                                            Synthetic antimicrobial peptide, indolicidin.
                                                                                                                                                                                                                                                        Mismatches
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0
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                                                                                                                                                                                                                                                                       29-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                 1 ILPWKWPWWRR 13
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Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                      Sequence 13 AA;
                                                                                                                                                                                                                                                                                                          AAY92794;
                                                                                                                                                                                                                                                                                         RESULT 13
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Gaps ô

100.0%; Score 99; DB 3; Length 13; 100.0%; Pred. No. 1.4e-06; ive 0; Mismatches 0; Indels

1 ILPWKWPWWRR 13

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1 ILPWKWPWWRR 13

Query Match Best Local Similarity 100. Matches 13; Conservative

AAY55056 standard; peptide; 13 AA.

RESULT 12 AAY55056 ID AAY5 XX

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Indolicidin, ophthalmic; disinfection; contact lens; antimicrobial; Pseudomonas aeruginosa; Staphylococcus aureus; Serratia marcescens; Candida albicans; Fusarium solani.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 99; DB 4; Length 13; 100.0%; Pred. No. 1.4e-06; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP60382 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indolicidin peptide SEQ ID NO 1.
                                                  17-MAY-2000; 2000WO-US013576.
                                                                                   99US-0134406P
                                                                                                99US-0153406P.
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nes 13; Conservative
                                                                                                                                                                         Ezrin AM,
                                                                                                                                            (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                        WPI; 2001-112059/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13 AA;
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                                                                              17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
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Modified-site
                     23-NOV-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indolicidin is a potent antimicrobial tridecapeptide, originally purified from cytoplasmic granules of bovine neutrophils. A reverse peptide, Rev4 (AAY92796) of indolicidin was found to have increased stability against plant protease degradation. Expression of antimicrobial peptides in transgenic plants suffers a major limitation in that the foreign peptides are susceptible to rapid degradation by proteases. The invention concerns produced by a plant by administering indolicidin, Rev4 or a functional produced by a plant by administering indolicidin, Rev4 or a functional Rev4 are useful for production of the antimicrobial peptides. Compositions containing indolicidin and Rev4 are useful for production of the antimicrobial peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protection, endogenous therapeutic peptide; peptidase, conjugation, blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                                      Polypeptides for reducing proteolytic degradation of proteins administered to, or produced by a plant comprise indolicin or its functional equivalents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
indolicidin; protein production; reverse peptide.
                                                                                                                                                                                                                                                                                                                             Lawrence C, Davies MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                           (INTE-) INTERLINK BIOTECHNOLOGIES LLC. (KENT ) UNIV KENTUCKY RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial peptide SEQ ID NO:1018.
                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 15; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB91842 standard; peptide; 13 AA.
                                                                                                           /note= "amidated'
                                                                                                                                                                                                    99WO-US025561
                                                                                                                                                                                                                                98US-0106373P
98US-0106537P
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                                                                                                                                        WO200026344-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13 AA;
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                                                                               Key
Modified-site
                                                                                                                                                                                                    29-OCT-1999;
                                                                                                                                                                                                                                30-OCT-1998;
02-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                           Everett NP,
                                                                                                                                                                    11-MAY-2000
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                                Bos taurus
                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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Best Loc Matches

ઠ g RESULT 14 AAB91842

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Gaps

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The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidy) and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3.50 amino acids.

(I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.

Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases

Iffe) and specificity as bonding to large molecules decreases

intracellular uptake and interference with physiological processes.

ARBO829 to AAB9241 represent peptides which can be used in the exemplification of the present invention
                                                                                                                                                                                                                                 Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.
      Thibaudeau K;
      Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 528; 733pp; English.
Milner PG,
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The invention relates to an ophthalmic composition (I) for storing, cleaning, or disinfecting a contact lens, comprising an indolicidin cleaning, or disinfecting a contact lens, comprising an indolicidin less than 0.85 weight's, based on the total weight of (I) or Good's buffer. (I) is a multipurpose solution for care of a contact lens and is suitable for contact lens disinfection, storage, cleaning, conditioning, rehydrating, moistening and lubricating (I) is useful for disinfecting the contact lens or contact lens storage vessel such as contact lens vial, contact lens or contact lens storage vessel such as contact lens vial, contact lens or exercise the shipping package by contacting the lens or vessel with a disinfecting solution comprising (I). (I) is useful for packaging a contact lens involving sealing the lens in a container with (I), where the contact lens is not autoclaved. (I) reduces the number of pseudomonas aeruginosa, Staphylococcus aureus and Serratia marcescens organisms by 3.0 logs or more within 4 hours and the number of candida albicans and Fusarium solani by 1.0 log or more within 18 hours. (I) is call-preserving and requires no additional preservatives or callination to the eye. (I) enables immediate application of the contact lens to the eye components of (I). The present sequence is that of an indolicidin peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                         Ophthalmic composition for storing, cleaning, or disinfecting contactens, comprises indolicidin, and buffer having specified halide ion concentration or Good's buffer.
                                                                                                                                                                                                                                                                                                 Hokama LA, Selsted ME, Chapoy LL,
                                                                            LARGE SCALE BIOLOGY CORP. SRI INT. UNIV CALIFORNIA. WESLEY-JESSEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 15; Page 68; 91pp; English.
23-MAY-2000; 2000WO-US014608.
                                        99US-00318195
                                                                                                                                                                     MORTELMANS K.
HOKAMA L A.
SELSTED M E.
CHAPOY L L.
QUINN M H.
                                                                                                                                                                                                                                                                                              Mortelmans K,
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